

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:05:20 ; Search time 11.62 Seconds

(without alignments)  
380.289 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLRFYVFLKGLTAAQ.....PPSFAYGKGYDKPLLAAGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 199.5 | 28.6        | 140    | 1     | FKB2_MOUSE  |
| 2          | 195.5 | 28.0        | 217    | 1     | FKB2_NEUCR  |
| 3          | 188.5 | 27.0        | 141    | 1     | FKB2_HUMAN  |
| 4          | 182   | 26.1        | 581    | 1     | FKB2_MOUSE  |
| 5          | 176.5 | 25.3        | 135    | 1     | FKB2_YEAST  |
| 6          | 144   | 20.6        | 114    | 1     | FKBP_YEAST  |
| 7          | 142.5 | 20.4        | 223    | 1     | FKB3_RABIT  |
| 8          | 142.5 | 20.4        | 224    | 1     | FKB3_BOVIN  |
| 9          | 142.5 | 20.4        | 392    | 1     | FKB4_YEAST  |
| 10         | 142   | 20.3        | 120    | 1     | FKBP_NEUCR  |
| 11         | 139.5 | 20.0        | 224    | 1     | FKB3_HUMAN  |
| 12         | 139.5 | 20.0        | 224    | 1     | FKB3_MOUSE  |
| 13         | 138.5 | 19.8        | 124    | 1     | FKBP_CANAL  |
| 14         | 135.5 | 19.4        | 101    | 1     | FKB1_DROME  |
| 15         | 135.5 | 19.4        | 411    | 1     | FKB3_YEAST  |
| 16         | 134   | 19.2        | 559    | 1     | FKB7_WHEAT  |
| 17         | 133.5 | 19.1        | 109    | 1     | FKBP_NEIMA  |
| 18         | 133.5 | 19.1        | 109    | 1     | FKBP_NEIMA  |
| 19         | 133   | 19.1        | 107    | 1     | FKB1_BOVIN  |
| 20         | 132.5 | 19.0        | 457    | 1     | FKB5_HUMAN  |
| 21         | 131   | 18.8        | 457    | 1     | FKB1_RABIT  |
| 22         | 130.5 | 18.7        | 107    | 1     | FKB1_RAT    |
| 23         | 130   | 18.6        | 107    | 1     | FKB1_HUMAN  |
| 24         | 129.5 | 18.6        | 412    | 1     | FKB4_SPOPR  |
| 25         | 128.5 | 18.4        | 112    | 1     | FKBP_SCHRO  |
| 26         | 128.5 | 18.4        | 357    | 1     | FKB4_DROME  |
| 27         | 124.5 | 17.8        | 456    | 1     | FKB5_MOUSE  |
| 28         | 124   | 17.8        | 107    | 1     | FKB1_MOUSE  |
| 29         | 124   | 17.8        | 124    | 1     | FKBP_STRCH  |
| 30         | 124   | 17.8        | 458    | 1     | FKB4_MOUSE  |
| 31         | 122.5 | 17.6        | 231    | 1     | FKB2_METYA  |
| 32         | 122   | 17.5        | 459    | 1     | FKB4_HUMAN  |
| 33         | 119   | 17.0        | 107    | 1     | FKB1_XENLA  |

## ALIGNMENTS

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 119   | 17.0 | 107 | 1 | FKB8_RAT   | P97534 rattus norv |
| 35 | 116   | 16.6 | 107 | 1 | FKB8_HUMAN | Q16645 homo sapien |
| 36 | 111   | 15.9 | 361 | 1 | FKB4_SCHPO | O74191 schizosacch |
| 37 | 104.5 | 15.0 | 157 | 1 | FKB1_METYA | O57726 methanococc |
| 38 | 103   | 14.8 | 362 | 1 | YAV6_SCHPO | Q10175 schizosacch |
| 39 | 100.5 | 14.4 | 268 | 1 | FKB4_AERHY | O08437 aeromonas h |
| 40 | 97.5  | 14.0 | 230 | 1 | MIP_COXBU  | P51752 coxiella bu |
| 41 | 95.5  | 13.7 | 154 | 1 | FKBP_METTL | O52980 methanococc |
| 42 | 89.5  | 12.8 | 270 | 1 | FKB4_ECOLI | P45523 escherichia |
| 43 | 88.5  | 12.7 | 243 | 1 | MIP_LEBMT  | P31106 legionella  |
| 44 | 88    | 12.6 | 205 | 1 | FKB8_ECOLI | P39311 escherichia |
| 45 | 87.5  | 12.5 | 241 | 1 | FKB9_HAEIN | P44760 haemophilus |

RESULT 1  
FKB2\_MOUSE STANDARD; PRT; 140 AA.  
AC P45878;  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 38, Last annotation update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE FK506-BINDING PROTEIN PRECURSOR (FKBP-13) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8).  
GN FKBP2 OR FKBP13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI-TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVJ; TISSUE=Liver;  
RX MEDLINE=94085790; PubMed=7505249;  
RA Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bieder R.E., Burakoff S.J., Dillella A.G.;  
RT "Structural organization of the genes encoding human and murine FK506-binding protein (FKBP) 13 and comparison to FKBP1.";  
RT Gene 134:271-275(1993).  
CC -!- FUNCTION: PIPIASES ACCELERATE THE FOLDING OF PROTEINS.  
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN, MEMBRANE ASSOCIATED (PROBABLE).  
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: M77831; AAA37631.1; -.  
CC HSSP: P20081; IYAT.  
CC MGD: MGI:95542; Fkbp2.  
CC InterPro: IPR001179; -.  
CC Pfam: PF00254; FKBP.1.  
CC PROSITE: PS00453; FKBP\_PIPIASE.1.  
CC PROSITE: PS00454; FKBP\_PIPIASE.2; 1.  
CC PROSITE: PS50059; FKBP\_PIPIASE.3; 1.  
CC Isomerase; Notamase; Signal; Endoplasmic reticulum.  
CC SIGNAL 1  
CC CHAIN 23 140 POTENTIAL.  
CC SITE 137 140 FK506-BINDING PROTEIN.  
CC FT PREVENT SECRETION FROM ER (POTENTIAL).  
CC SEQUENCE 140 AA; 15344 MM; F4E7FCCT766A0416 CRC64;

Query Match 28.6%; Score 199.5; DB 1; Length 140;  
Best local Similarity 46.8%; Pred. No. 1,9e-13;

| Matches               | 44: Conservative   | 15: Mismatches  | 32: Indels         | 3: Gaps                                | 2           |
|-----------------------|--|---|--------------------|--|-------------|
| QY                    | 26   | ESTEEVAKIEVLHPENCSTKSKGDLINAHYDGLADGSGFYTCSRFQNECHGPKWFLVGV   | 85                 |  |             |
| DB                    | 24   | EGKRRKLGIVYKRRVDDHCPPIKSRKGDVLMHMTGTL-DEGTEFSSLLPQNO--PVFSLGT | 80                 |  |             |
| QY                    | 86   | GVVTKGDLIAMTDMCPEKRRKVVIPSPAYKREG                             | 119                |  |             |
| DB                    | 81   | GVVTKGMDGLGMCCEKRRKVVIPSELGYOERG                              | 114                |  |             |
| RESULT                | 2  |   |                    |  |             |
| ID                    | FK21_NEUCR   | STANDARD:   | PRT:               | 217 AA.                                |             |
| AC                    | 060046:  |   |                    |  |             |
| DT                    | 15-DEC-1998 (Rel. 37, Created)   |   |                    |  |             |
| DT                    | 15-DEC-1998 (Rel. 37, Last sequence update)  |   |                    |  |             |
| DT                    | 15-JUL-1999 (Rel. 38, Last annotation update)  |   |                    |  |             |
| DE                    | FK506-BINDING PROTEIN PRECURSOR (FKBP-21) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8).                  |   |                    |  |             |
| DE                    | FKBP-21.   |   |                    |  |             |
| OS                    | Neurospora crassa.   |   |                    |  |             |
| OC                    | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;   |   |                    |  |             |
| OC                    | Sordariales; Sordariaceae; Neurospora.   |   |                    |  |             |
| OX                    | NCBI_TaxID=5141;   |   |                    |  |             |
| RN                    | [1]  |   |                    |  |             |
| RP                    | SEQUENCE FROM N.A.   |   |                    |  |             |
| RC                    | STRAIN=74-OR23-1A;   |   |                    |  |             |
| RA                    | Solscheid B.; Tropeschug M.;   |   |                    |  |             |
| CC                    | Submitted (May-1998) to the EMBL/Genbank/DBJ databases.  |   |                    |  |             |
| CC                    | -1- FUNCTION: PIPIASES ACCELERATE THE FOLDING OF PROTEINS.   |   |                    |  |             |
| CC                    | -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  |   |                    |  |             |
| CC                    | PEPTIDE BONDS IN OLIGOPEPTIDES.  |   |                    |  |             |
| CC                    | -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.   |   |                    |  |             |
| CC                    | -----  |   |                    |  |             |
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| CC                    | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |   |                    |  |             |
| CC                    | -----  |   |                    |  |             |
| DR                    | EMBL, AJ006297; CA006962.1; -  |   |                    |  |             |
| DR                    | InterPro; IPR000886; -   |   |                    |  |             |
| DR                    | InterPro; IPR001179; -   |   |                    |  |             |
| DR                    | Pfam; PF00254; FKBP; 1.  |   |                    |  |             |
| DR                    | PROSITE; PS00453; FKBP_PIPIASE_1; FALSE_NEG.   |   |                    |  |             |
| DR                    | PROSITE; PS00454; FKBP_PIPIASE_2; 1.   |   |                    |  |             |
| DR                    | PROSITE; PS50059; FKBP_PIPIASE_3; 1.   |   |                    |  |             |
| DR                    | PROSITE; PS00014; ER_TARGET; 1.  |   |                    |  |             |
| DR                    | Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.  |   |                    |  |             |
| FT                    | SIGNAL   | 1   | 20                 | POTENTIAL.                             |             |
| FT                    | CHAIN  | 21  | 217                | FK506-BINDING PROTEIN.                 |             |
| FT                    | SITE   | 214   | 217                | PREVENT SECRETION FROM ER (POTENTIAL). |             |
| SEQ                   | SEQUENCE   | 217 AA;   | 22915 MW;          | 72313067521BCDAF CRC64;                |             |
| Query Match           |  | 28.0%;  | Score 195.5;       | DB 1;                                  | Length 217; |
| Best Local Similarity |  | 45.1%;  | Pred. No. 7.8e-13; |  |             |
| Matches               | 41;  | Conservative  | 15;                | Mismatches                             | 32;         |
|                       |  |   |                    | Indels                                 | 3;          |
|                       |  |   |                    | Gaps                                   | 2           |
| QY                    | 27   | STEEVAKIEVLHPENCSTKSKGDLINAHYDGLADGSKFYSRFQNECHGPKWFLVGVG     | 86                 |  |             |
| DB                    | 20   | AABELGDIATV-VEVEDCKRTRKCDKRNHVRGLQSGQGFDA--YDRGTPPSFKLGSG     | 76                 |  |             |
| QY                    | 87   | GVVTKGDLIAMTDMCPEKRRKVVIPSPAYK                                | 117                |  |             |
| DB                    | 77   | GVVTKGDEGLVDMCIGEKRTLIVPPSYGQ                                 | 107                |  |             |
| RESULT                | 3  |   |                    |  |             |

| ID | FKB2_HUMAN  | STANDARD; | PRT; | 141 AA. |
|----|---|-----------|------|---------|
| AC | P26885;   |           |      |         |
| DT | 01-AUG-1992 (Rel. 23, Created)  |           |      |         |
| DT | 01-AUG-1992 (Rel. 23, last sequence update)   |           |      |         |
| DT | 15-JUL-1999 (Rel. 38, last annotation update)   |           |      |         |
| DE | FK506-BINDING PROTEIN PRECURSOR (FKBP-13) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8).  |           |      |         |
| DE | FKBP2 OR FKBP13.  |           |      |         |
| OS | Homo sapiens (Human).   |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.   |           |      |         |
| OC | NCBI_TaxID=9606;  |           |      |         |
| OX | [1]   |           |      |         |
| RN | SEQUENCE FROM N.A.  |           |      |         |
| RP | TISSUE-Colon carcinoma;   |           |      |         |
| RC | MEDLINE=91319747; PubMed=1713687;   |           |      |         |
| RX | Jin Y.-J., Albers M.W., Lane W.S., Blierer B.E., Schreiber S.L., Birkhoff S.J.;   |           |      |         |
| RA | "Molecular cloning of a membrane-associated human FK506- and rapamycin-binding protein. FKBP-13."   |           |      |         |
| RT | Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991).   |           |      |         |
| RL | [2]   |           |      |         |
| RX | SEQUENCE FROM N.A.  |           |      |         |
| RA | Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.;   |           |      |         |
| RT | "Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13."   |           |      |         |
| RL | Biochem. Biophys. Res. Commun. 189:819-823(1992).   |           |      |         |
| CC | -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.   |           |      |         |
| CC | -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.   |           |      |         |
| CC | -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.   |           |      |         |
| CC | -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLY).  |           |      |         |
| CC | -1- TISSUE SPECIFICITY: T-CELLS AND THYMUS.   |           |      |         |
| CC | -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.   |           |      |         |
| CC | -----   |           |      |         |
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| CC | -----   |           |      |         |
| DR | EMBL; M65128; AAA58473.1; -   |           |      |         |
| DR | EMBL; M75099; AAA36563.1; -   |           |      |         |
| DR | PIR; JC1365; JC1365.  |           |      |         |
| DR | HSSP; P20071; 1FKT.   |           |      |         |
| DR | MM; 186946; -   |           |      |         |
| DR | InterPro; IPR001179; -  |           |      |         |
| DR | Pfam; PF00254; FKBP, 1.   |           |      |         |
| DR | PROSITE; PS00453; FKBP_PPIASE.1; 1.   |           |      |         |
| DR | PROSITE; PS00454; FKBP_PPIASE.2; 1.   |           |      |         |
| DR | PROSITE; PS50059; FKBP_PPIASE.3; 1.   |           |      |         |
| KW | Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.   |           |      |         |
| FT | SIGNAL 1 21   |           |      |         |
| FT | CHAIN 22 141  |           |      |         |
| FT | SITE 138 141  |           |      |         |
| FT | VARIANT 21 21   |           |      |         |
| FT | VARIANT 24 24   |           |      |         |
| FT | VARIANT 96 96   |           |      |         |
| FT | SEQUENCE 141 AA; 15654 MW; 9FA751CA7D82D064 CRC64;  |           |      |         |
| FT | FTId=VAR_006412.  |           |      |         |
| FT | FTId=VAR_006411.  |           |      |         |
| FT | FTId=VAR_006410.  |           |      |         |
| FT | FTId=VAR_006409.  |           |      |         |
| FT | FTId=VAR_006408.  |           |      |         |
| FT | FTId=VAR_006407.  |           |      |         |
| FT | FTId=VAR_006406.  |           |      |         |
| FT | FTId=VAR_006405.  |           |      |         |
| FT | FTId=VAR_006404.  |           |      |         |
| FT | FTId=VAR_006403.  |           |      |         |
| FT | FTId=VAR_006402.  |           |      |         |
| FT | FTId=VAR_006401.  |           |      |         |
| FT | FTId=VAR_006400.  |           |      |         |
| FT | FTId=VAR_006399.  |           |      |         |
| FT | FTId=VAR_006398.  |           |      |         |
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| FT | FTId=VAR_006389.  |           |      |         |
| FT | FTId=VAR_006388.  |           |      |         |
| FT | FTId=VAR_006387.  |           |      |         |
| FT | FTId=VAR_006386.  |           |      |         |
| FT | FTId=VAR_006385.  |           |      |         |
| FT | FTId=VAR_006384.  |           |      |         |
| FT | FTId=VAR_006383.  |           |      |         |
| FT | FTId=VAR_006382.  |           |      |         |
| FT | FTId=VAR_006381.  |           |      |         |
| FT | FTId=VAR_006380.  |           |      |         |
| FT | FTId=VAR_006379.  |           |      |         |
| FT | FTId=VAR_006378.  |           |      |         |
| FT | FTId=VAR_006377.  |           |      |         |
| FT | FTId=VAR_006376.  |           |      |         |
| FT | FTId=VAR_006375.  |           |      |         |
| FT | FTId=VAR_006374.  |           |      |         |
| FT | FTId=VAR_006373.  |           |      |         |
| FT | FTId=VAR_006372.  |           |      |         |
| FT | FTId=VAR_006371.  |           |      |         |
| FT | FTId=VAR_006370.  |           |      | </      |

OY 26 ESTEYKLEVLHRRPENCSTKSGDGLNHAHYDGLAKDSEKFCYSTRONCHGPKWFLVGLV 85  
 DB 25 EGKRLQIGVKKRVDHCPKRSKRGDVLHMYTKGL-EDGTEFSDSLPQNG--PFFVSLGT 81  
 OY 86 GOVTKGLDIAWDMCPEKRRVIPPSPAYGKEG 119  
 DB 82 GOVTKGMDGLGMEGKRLVTPSELGVEG 115

RESULT 4  
 ID FKBP\_MOUSE STANDARD: PRT: 581 AA.  
 AC 061576:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP)  
 DE (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (ROTAMASE)  
 DE (IMMUNOPHILIN FKBP65)  
 GN FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J6; TISSUE=Epidermis;  
 RA MEDLINE=94117013; PubMed=7507077;  
 RA Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;  
 RT "Sequence and localization of a novel FK506-binding protein to mouse  
 RT chromosome 11";  
 RL Genomics 18:407-409(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RA MEDLINE=96094328; PubMed=7493967;  
 RA Coss M.C., Winterstein D., Sowder R.C., Simek S.L.;  
 RT "Molecular cloning, DNA sequence analysis, and biochemical  
 RT characterization of a novel 65-kDa FK506-binding protein (FKBP65).";  
 RL J. Biol. Chem. 270:29336-29341(1995).  
 CC -1- FUNCTION: PIPASE ACCELERATE THE FOLDING OF PROTEINS DURING  
 CC PROTEIN SYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT  
 CC BY CYCLOSPORINE A.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASTIC RETICULUM (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN  
 CC AND TESTIS.  
 CC -1- PTM: GLYCOSYLATED AND PHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY. CONTAINS 4  
 CC FKBP-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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 CC  
 CC -----  
 CC EMBL, L07063; AAC37678.1; -  
 CC MGD; MGI:104769; FKBP6.  
 CC InterPro: IPR000886; -  
 CC InterPro: IPR001179; -  
 CC InterPro: IPR002048; -  
 CC Pfam: PF00254; FKBP; 4.  
 CC Pfam: PF00036; efhand; 2.  
 CC PROSITE: PS00453; FKBP\_PIPIASE\_1; FALSE\_NEG.  
 CC PROSITE: PS00454; FKBP\_PIPIASE\_2; 1.  
 CC PROSITE: PS00509; FKBP\_PIPIASE\_3; 4.  
 CC PROSITE: PS00014; ER\_TARGET; 1.  
 CC PROSITE: PS00018; EF\_HAND; 1.

KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;  
 KM Endoplasmic reticulum; Calcium binding.  
 FT SIGNAL 1 33  
 FT CHAIN 34 581  
 FT DOMAIN 54 146  
 FT DOMAIN 179 258  
 FT DOMAIN 291 370  
 FT DOMAIN 389 482  
 FT CA\_BIND 509 520  
 FT CA\_BIND 554 565  
 FT CARBOHYD 69 69  
 FT CARBOHYD 181 181  
 FT CARBOHYD 293 293  
 FT CARBOHYD 309 309  
 FT CARBOHYD 351 351  
 FT CARBOHYD 392 392  
 FT CARBOHYD 406 406  
 FT SITE 578 581  
 SQ SEQUENCE 581 AA; 64669 MW; 1B51B3032089E555 CRC64;

Query Match 26.1%; Score 182; DB 1; Length 581;  
 Best Local Similarity 37.9%; Pred. No. 5,5e-11;  
 Matches 39; Conservative 24; Mismatches 30; Indels 10; Gaps 4;

OY 28 TEEVKLEVLHRR-PEKSKTKSKGDLNHAHYDGLAKDSEKFCYSTRONCHGPKWFLVGLV 86  
 DB 376 SDVEKTKTLSPKENCNEKSGIDFRTYHNCSL-DGRLRSSHYEA--POEITGLAN 432

OY 87 QVTKGLDIAWDMCPEKRRVIPPSPAYGKEGYDKPLAKGI 129  
 DB 433 KVLEGIDRLGQKWCGERQLIVPPLAHGENG-----ARGCV 469

RESULT 5  
 ID FKBP\_YEAST STANDARD: PRT: 135 AA.  
 AC P32472:  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-BINDING PROTEIN PRECURSOR (FKBP-13) (FKBP-15) (PEPTIDYL-PROLYL  
 DE CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8).  
 GN PPR2 OR FKBP2 OR YDR519W OR D9719.24.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93070605; PubMed=1279908;  
 RA Parlatadis J.A., Fleming M.A., Harding M.W., Berlin V.;  
 RT "Saccharomyces cerevisiae contains a homolog of human FKBP-13, a  
 RT membrane-associated FK506/rapamycin binding protein.";  
 RL Yeast 8:673-680(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-54.  
 RA MEDLINE=92366483; PubMed=1380159;  
 RA Nielsen J.B., Poor F., Stiekerka J.J., Hsu M.J., Ramadan N.,  
 RA Morlin N., Shafiee A., Dahl A., Brizuela L., Chretien G.,  
 RA Bostian K.A., Parent S.A.;  
 RT "Yeast FKBP-13 is a membrane-associated FK506-binding protein encoded  
 RT by the nonessential gene FKBP2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7471-7475(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,  
 RA Benito A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,  
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Moseley D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,  
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,  
 RA Winant A., Yelton M., Botstein D., Davis R.W.;  
 RL submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

```

CC -1- FUNCTION: PIPIASES ACCELERATE THE FOLDING OF PROTEINS. FKBP-13 MAY
CC PLAY A ROLE IN PROTEIN TRAFFICKING IN THE ER.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC BINDS FK506 WITH 15-FOLD LOWER AFFINITY THAN FKBL.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. IS NOT SECRETED AND
CC PROBABLY LOCALIZED IN THE ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.
CC
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CC -----
CC EMBL: M90646; AAA34604.1; -
CC EMBL: M90767; AAA34605.1; -
CC EMBL: U33057; AAB64960.1; -
CC PIR: S25337; S25337.
CC PIR: A46154; A46154.
CC HSSP: P20081; 1YAT.
CC SGD: S0002927; FKBP.
CC InterPro: IPR001179; -
CC DR PIR: PF00254; FKBP_PPIASE_1; 1.
CC PROSITE: PS00453; FKBP_PPIASE_1; 1.
CC PROSITE: PS00454; FKBP_PPIASE_2; 1.
CC DR PROSITE: PS50059; FKBP_PPIASE_3; 1.
CC KM Isomerase; Rotamase; Signal; Endoplasmic reticulum.
CC FT SIGNAL 1 17 FK506-BINDING PROTEIN.
CC CHAIN 18 135
CC SEQUENCE 135 AA; 14487 MW; 09CA3F1568D7E4B4 CRC64;
SQ
Query Match 25.3%; Score 176.5; DB 1; Length 135;
Best Local Similarity 36.6%; Pred. No. 3.9e-11;
Matches 45; Conservative 19; Mismatches 42; Indels 17; Gaps 4;
OY 1 MHFFRTFVF--YLMGLFTAQRKKESTEEVKEIEVLR--PENCSKTSKGGDLNANY 56
Db 2 MENIYLFVTFSTILAG-----SLSDLEIGIKRPVDCILKAMPGBKRVAVY 50
OY 57 DGYLANQSKRYCYCRTONEGHPKRVFVGVGYVITGLDIAMDQPGKRVVIPPSPAYG 116
Db 51 TGSLEISGVF--DSSYSRGSPIAFELGVGVKGVKMDQGVAGKCVGERKRLDIPSSLAYG 108
OY 117 KEG 119
Db 109 ERG 111

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RT cerevisiae and contains regions suggesting homology to the
RT cyclophilins."
RT Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033(1991).
RT [2]
RT RP SEQUENCE FROM N.A.
RT MEDLINE=91156723; PubMed=1705713;
RT Heltman J., Movva R.N., Hiestand P.C., Hall M.N.;
RT "FK 506-binding protein proline rotamase is a target for the
RT immunosuppressive agent FK 506 in Saccharomyces cerevisiae."
RT Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952(1991).
RT [3]
RT RP SEQUENCE FROM N.A.
RT MEDLINE=91141524; PubMed=1996117;
RT Kollin Y., Faucette L., Bergsma D.J., Levy M.A., Cafferty R.,
RT Koser P.L., Johnson R.K., Livi G.P.;
RT "Rapamycin sensitivity in Saccharomyces cerevisiae is mediated by a
RT peptidyl-prolyl cis-trans isomerase related to human FK506-binding
RT protein."
RT Mol. Cell. Biol. 11:1718-1723(1991).
RT [4]
RT RP SEQUENCE FROM N.A.
RT STRAIN=S288C;
RT MEDLINE=96109932; PubMed=8619318;
RT Mallet L., Busseureau F., Jaquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
RT MEP2, CAP/SRV2, NAM9, FKBL/PP1/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames."
RT Yeast 11:1195-1209(1995).
RT [5]
RT RP SEQUENCE OF 67-100.
RT MEDLINE=91065908; PubMed=1701173;
RT Stieklerka J.J., Wiedrecht G., Greulich H., Boulton D., Hung S.H.Y.,
RT Cryan J., Hodges P.J., Sigal N.H.;
RT "The cytosolic-binding protein for the immunosuppressant FK-506 is
RT both a ubiquitous and highly conserved peptidyl-prolyl cis-trans
RT isomerase."
RT J. Biol. Chem. 265:21011-21015(1990).
RT [6]
RT RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RT MEDLINE=93216714; PubMed=7681823;
RT Rotondo J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;
RT "Improved calcineurin inhibition by yeast FKBP12-drug complexes.
RT Crystallographic and functional analysis."
RT J. Biol. Chem. 268:7607-7609(1993).
RT [7]
RT CC -1- FUNCTION: PIPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND
CC ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.
CC
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CC -----
CC EMBL: Z46843; CAA86890.1; -
CC EMBL: M57967; AAA34564.1; -
CC EMBL: M60877; AAA34607.1; -
CC EMBL: M63892; AAA34962.1; -
CC EMBL: 271411; CAA96017.1; -
CC PIR: A33146; A33146.
CC PIR: A37870; A37870.
CC PIR: A39122; A39122.
CC PIR: C38333; C38333.
CC PIR: S13758; S13758.
CC PDB: 1YAT; 31-OCT-93.
CC SGD: S0005079; PP1.
CC InterPro: IPR001179; -

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|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 20.68; | Score 144;         | DB 1;  | Length 114;    |
| Best Local Similarity | 38.9%; | Pred. No. 6.5e-08; |        |                |
| Matches               | 35;    | Conservative       | 17;    | Mismatches 34; |
|                       |        |                    | Indels | 4;             |
|                       |        |                    | Gaps   | 3              |

|  |  |           |      |         |  |
|--|--|-----------|------|---------|--|
|  | RESULT   | 7         |      |         |  |
|  | FKB3_RABIT   |           |      |         |  |
| ID   | FKB3_RABIT   | STANDARD: | PRT; | 223 AA. |  |
| AC   | 046638;  |           |      |         |  |
| DT   | 15-JUL-1999 (Rel. 38, Created)                                       |           |      |         |  |
| DR   | 15-JUL-1999 (Rel. 38, Last sequence update)                          |           |      |         |  |
| DT   | 15-JUL-1999 (Rel. 38, Last annotation update)                        |           |      |         |  |
| DE   | RAPAMYCIN-SELECTIVE 25 KDA IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL    |           |      |         |  |
| DE   | CIS--TRANS ISOMERASE) (EC 5.2.1.8) (PPINASE) (ROTAMASE) (FRAGMENT) . |           |      |         |  |
| OS   | FKBP3 OR FKBP25.   |           |      |         |  |
| GN   | Oryctolagus cuniculus (Rabbit).                                      |           |      |         |  |
| OC   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |           |      |         |  |
| OX   | Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctologus,              |           |      |         |  |
| NCBI_TaxId   | 9986;  |           |      |         |  |
| [1]  |  |           |      |         |  |
| SEQUENCE FROM N.A.   |  |           |      |         |  |
| TISSUE=Cornea;   |  |           |      |         |  |
| MEDLINE=97030438; PubMed=8876379;                                |  |           |      |         |  |
| Kitagawa H., Hotta Y., Fujiki K., Kanai A.;                      |  |           |      |         |  |
| "Cloning and high expression of rabbit FKBP25 in cornea."        |  |           |      |         |  |
| Jpn. J. Ophthalmol. 40:133-141(1996).                            |  |           |      |         |  |
| -1 FUNCTION: PIPASIS ACCELERATE THE FOLDING OF PROTEINS.         |  |           |      |         |  |
| -1 CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC |  |           |      |         |  |
| PEPTIDE BONDS IN OLIGOPEPTIDES.                                  |  |           |      |         |  |
| -1 ENZYME REGULATION: INHIBITED PREFERENTIALLY BY RAPAMYCIN OVER |  |           |      |         |  |
| FK306.   |  |           |      |         |  |

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|                          |        |                    |            |             |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match              | 20.48; | Score 142.5;       | DB 1;      | Length 223; |
| Best Local Similarity    | 36.98; | Pred. No. 1.9e-07; |            |             |
| Matches 41; Conservative | 19;    | Mismatches 32;     | Indels 19; | Gaps 5      |

| RESULT     | 8          |
|------------|------------|
| FKB3_BOVIN |            |
| ID         | FKB3_BOVIN |
| CC         | P26984     |
| STANDARD;  |            |
| PRT;       | 224 AA.    |

RC TISSUE=Brain, Thymus, and Spleen;  
RX MEDLINE=92172870; Pubmed=1371698;  
RA Galat A., lane W.S., Standert R.F., Schreiber S.L.;  
RT "A rapamycin-selective 25-kDa immunophilin";  
RL Biochemistry 31:2427-2434(1992).

- FUNCTION: FK506 AND RAPAMYCIN-BINDING PROTEINS (FKBP) CONSTITUTE A FAMILY OF RECEPTORS FOR THE TWO IMMUNOSUPPRESSANTS WHICH INHIBIT T CELL PROLIFERATION BY ARRESTING TWO DISTINCT CYTOPLASMIC SIGNAL TRANSMISSION PATHWAY.  
 - FUNCTION: PIPTASES ACCELERATE THE FOLDING OF PROTEINS.  
 - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 - ENZYME REGULATION: INHIBITED PREFERENTIALLY BY RAPAMYCIN OVER FK506.  
 - SUBCELLULAR LOCATION: MITOCHONDRIA.

-- SIMILARITY: BELONGS TO THE FRBP-TYPE PIASE FAMILY.

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DR EMBL: M95123; AAA30348.1; -  
 DR PIR: A40050; A40050.  
 DR PIR: A42212; A42212.  
 DR HSSP: Q00688; 1PBK.  
 DR InterPro: IPR001179; -  
 DR Pfam: PF00254; FKBP\_PPIASE\_1; 1.  
 DR PROSITE: PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE: PS00459; FKBP\_PPIASE\_3; 1.  
 DR Isomerase: Rotamase; Nuclear protein.  
 DR DOMAIN 128 224 PPIASE; FKBP-TYPE.  
 FT COMPLET 207 209 KIP -> IXO (IN REF. 2).  
 SQ SEQUENCE 224 AA; 25191 MW; 93DA5F8FB79A01FD CRC64;

Query Match 20.4%; Score 142.5; DB 1; Length 224;  
 Best Local Similarity 30.4%; Pred. No. 2e-07;  
 Matches 42; Conservative 24; Mismatches 37; Indels 35; Gaps 5;

OY 16 LFTAQROKKESTEEVKIEVLH-----RPENC-----SKTS-- 46  
 DB 66 LFESKRRKGTESISKVSEOVKNVKNLNEDEKPKETKSEETLDEGPKKTKSVLKKGDKTNFP 125  
 OY 47 KKGDLNAHYDGYLAKGSKF-----YCSPTONEGHPKFWVLGVOYIKGIDAMTDMCP 101  
 DB 126 KKGIVVCHWTGTL-ODGYVDTNIGTSSKKKKNAKPLSEKVGIGKVIKGMDEALLTMSK 184  
 OY 102 GKKRVVIPPSPFAYGKEG 119  
 DB 185 GEKARLEIEPEMAYGKKG 202

RESULT 9  
 FKBP\_YEAST STANDARD; PRT; 392 AA.  
 ID FKBP\_YEAST  
 AC Q06205;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-BINDING PROTEIN 4 (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)  
 DE (PIRASE) (EC 5.2.1.8).  
 OS FPR4 OR YIR449W OR L9324.3.  
 ON Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SS288C / AB972;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
 RA Favella A., Fulton L., Gattung S., Greco T., Kirsten J.,  
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,  
 RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,  
 RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,  
 RA Rifken L., Riles L., Tatch A., Trevaskis E., Vignati D.,  
 RA Wilcox L., Wohlschlag P., Vaudin M., Wilson R., Waterston R.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases  
 CC -1 CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC -1 SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
 CC -1 SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC -----  
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DR EMBL: U22382; AAB67528.1; -  
 DR SGD: S000444; FPR4.  
 DR InterPro: IPR001179; -  
 DR Pfam: PF00254; FKBP; 1.  
 DR PROSITE: PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE: PS00459; FKBP\_PPIASE\_3; 1.  
 DR Isomerase; Rotamase; Nuclear protein.  
 DR DOMAIN 191 199 POLY-GLU.  
 FT SEQUENCE 392 AA; 43903 MW; CF90C6714F04572E CRC64;

Query Match 20.4%; Score 142.5; DB 1; Length 392;  
 Best Local Similarity 33.6%; Pred. No. 3.7e-07;  
 Matches 39; Conservative 17; Mismatches 39; Indels 21; Gaps 3;

OY 20 QROKKESTEEVKIEVLHNPENCKT-----SKGDLNAHYDGYLAK 62  
 DB 260 QTTKKDKNAEKYKDESESKPKPTKLEGIIEDRVTKGPKHAKKGTVMRYGKL-K 318  
 OY 63 DSKFYCSPTONEGHPKFWVLGVOYIKGIDAMTDMCPGKKRVVIPPSPFAYGKE 118  
 DB 319 NGKVF---DKNTKGRPFVFKIGQGEVIRKGMIDVAGMAVGGERIVIPAPYATGKQ 371

RESULT 10  
 FKBP\_NEUCR STANDARD; PRT; 120 AA.  
 ID FKBP\_NEUCR  
 AC P20080;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)  
 DE (PIRASE) (EC 5.2.1.8).  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Sordariales; Sordariaceae; Neurospora.  
 CX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90348972; PubMed=1696687;  
 RA Troschig M., Wächter E., Mayer S., Schoenbrunner E.R., Schmid F.X.;  
 RT Isolation and sequence of an FK506-binding protein from N. crassa  
 RL which catalyzes protein folding.";  
 RL Nature 346:674-677(1990).  
 CC -1 FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.  
 CC -1 CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1 SUPPLEMENTARY BINDING: BELONGS TO THE IMMUNOSUPPRESSANT DRUG FK506.  
 CC -1 SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC -----  
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DR EMBL: X55743; CAA39274.1; -  
 DR PIR: S11090; S11090.  
 DR HSSP: P20071; 1FKK.  
 DR InterPro: IPR001179; -  
 DR Pfam: PF00254; FKBP; 1.  
 DR PROSITE: PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE: PS00459; FKBP\_PPIASE\_3; 1.  
 DR Isomerase; Rotamase.  
 FT SEQUENCE 120 AA; 13037 MW; AF97183C0A1563B7 CRC64;

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CC      EMBL: M96256; AAA58471.1; -
DR      EMBL: M90309; AAA58475.1; -
DR      EMBL: M90820; AAA58474.1; ALT_FRAME.
DR      PIR: J01522; J01522.
DR      PDB: 1PBK; 14-OCT-96.
DR      MIM: 186947; -.
DR      InterPro: IPR001179; -.
DR      Pfam: PF000254; FKBP.1.
DR      PROSITE: PS00453; FKBP_PPIASE_1; 1.
DR      PROSITE: PS00454; FKBP_PPIASE_2; 1.
DR      PROSITE: PS50059; FKBP_PPIASE_3; 1.
KW      Isomerase; Rotamase; Nuclear protein; 3D-structure.
FT      DOMAIN 128 224 protein, FKBP-type.
FT      CONFLICT 181 181 T->A (IN REF.3).
SQ      SEQUENCE 224 AA; 25177 MW; C144C5AAB7EA9522 CRC64;

Query Match          20.0%; Score 139.5; DB 1; Length 224;
Best Local Similarity 30.4%; Pred. No. 3,9e-07;
Matches 42; Conservative 23; Mismatches 38; Indels 35; Gaps 5;

QY      16 LFTAOROKKESTEETVKYIEVLH-----RPENC-----SKTS-- 46
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      66 LPETRKFRGTSEISIKVSQYKVKVLNEDKPKETKSEETLDEGPPKYTKVLKGGKPTNEP 125
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      47 KKGDDLNAHYDSYLAKDSSKF-----YCSRONEGHPKWPFLYGQVYIKGDIAMTMCPR 101
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      126 KKGDDVHCWYGTGL-QDGTTFEDFTNIQTSAKKKKKNAKPLSPFKVGKYLIGWDALLTMSK 184
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      102 GERRKRVIPSPFAYGKEG 119
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      185 GEARLIEIEPWAYGKKG 202
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
FKB3_MOUSE          STANDARD;          PRT;          224 AA.
AC      062446; Q9WTU7;
DT      30-MAY-2000 (Rel. 39, Created)
DT      01-OCT-2000 (Rel. 40, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      RAAMYCIN-SELECTIVE 25 KDA IMMUNOPHILIN (FKBP25) (PPTIDYL-PROLYL
DE      CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE).
DE      GN FKBP3 OR FKBP25.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
      [1]
RN      RP
RP      SEQUENCE FROM N.A.
RN      RC
RC      TISSUE=Telencephalon;
RN      RA
RA      Mas C., Bourgeois F., Simonneau M.;
RT      "Isolation and mapping assignment of cDNAs differentially expressed in
RT      embryonic telencephalon."
RL      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
      [2]
RN      RP
RP      SEQUENCE FROM N.A.
RN      RC
RC      TISSUE=Telencephalon;
RN      RA
RA      Ahn J., Krawtowitz S., Murphy M., Wang A., Levine A.J., George D.L.;
RT      "Down-Regulation of the Statmin/Op18 and FKBP25 Genes Following p53
RT      Expression."
RL      Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
      [3]
RN      RP
RP      SEQUENCE OF 168-224 FROM N.A.
RN      RC
RC      MEDLINE=97115879; PubMed=8956998;
RN      RA
RA      Murphy M., Himman A., Levine A.J.;
RT      "Wild type p53 negatively regulates a microtubule associated
RT      protein."
RL      Genes Dev. 10:2971-2980(1996).
CC      - FUNCTION: FKBP25 AND RAAMYCIN-BINDING PROTEINS (FKBPs) CONSTITUTE
CC      A FAMILY OF RECEPTORS FOR THE TWO IMMUNOSUPPRESSANTS WHICH INHIBIT
CC      T CELL PROLIFERATION BY ARRESTING TWO DISTINCT CYTOPLASMIC SIGNAL
CC      TRANSDUCTION PATHWAYS.

```



[illegible]





Fri Aug 31 12:10:26 2001

us-09-622-522-1.rsp

Page 10

Job time: 98 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:04 ; Search time 21.29 Seconds

(Without alignments)  
367.332 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLFRFVFLYLMGLFTAAQ.....PPSPAYKGYDKPLKANGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

A\_Geneseq\_0601:\*

- 1: /SIDs8/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
- 2: /SIDs8/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
- 3: /SIDs8/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
- 4: /SIDs8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*
- 5: /SIDs8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*
- 6: /SIDs8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
- 7: /SIDs8/gcgdata/geneseq/geneseqp/AA1986.DAT:\*
- 8: /SIDs8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*
- 9: /SIDs8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*
- 10: /SIDs8/gcgdata/geneseq/geneseqp/AA1989.DAT:\*
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- 13: /SIDs8/gcgdata/geneseq/geneseqp/AA1992.DAT:\*
- 14: /SIDs8/gcgdata/geneseq/geneseqp/AA1993.DAT:\*
- 15: /SIDs8/gcgdata/geneseq/geneseqp/AA1994.DAT:\*
- 16: /SIDs8/gcgdata/geneseq/geneseqp/AA1995.DAT:\*
- 17: /SIDs8/gcgdata/geneseq/geneseqp/AA1996.DAT:\*
- 18: /SIDs8/gcgdata/geneseq/geneseqp/AA1997.DAT:\*
- 19: /SIDs8/gcgdata/geneseq/geneseqp/AA1998.DAT:\*
- 20: /SIDs8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
- 21: /SIDs8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*
- 22: /SIDs8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 698   | 100.0       | 129    | 20 | Transmembrane doma |
| 2          | 653   | 93.6        | 219    | 20 | Secreted protein e |
| 3          | 653   | 93.6        | 222    | 21 | Human PRO1304 prot |
| 4          | 653   | 93.6        | 222    | 21 | Human PRO1304 (UNQ |
| 5          | 653   | 93.6        | 222    | 22 | Protein of the inv |
| 6          | 653   | 93.6        | 222    | 22 | Human PRO1304 prot |
| 7          | 648   | 92.8        | 222    | 21 | Amino acid sequenc |
| 8          | 344   | 49.3        | 68     | 21 | Human 5' EST relat |
| 9          | 275   | 39.4        | 57     | 20 | Secreted protein e |
| 10         | 271.5 | 38.9        | 211    | 20 | Human PRO381 prote |
| 11         | 271.5 | 38.9        | 211    | 20 | Polypeptide fragme |

|    |       |      |     |    |                       |
|----|-------|------|-----|----|-----------------------|
| 12 | 271.5 | 38.9 | 211 | 21 | Human PRO381 (UNQ3    |
| 13 | 271.5 | 38.9 | 211 | 21 | Human PRO381 prote    |
| 14 | 271.5 | 38.9 | 211 | 21 | Human PRO381 prote    |
| 15 | 271.5 | 38.9 | 211 | 21 | Human secreted pro    |
| 16 | 271.5 | 38.9 | 211 | 22 | Human PRO381 prote    |
| 17 | 271.5 | 38.9 | 211 | 22 | Human PRO381 prote    |
| 18 | 271   | 38.8 | 186 | 20 | Polypeptide fragme    |
| 19 | 269.5 | 38.6 | 118 | 20 | Human embryonal li    |
| 20 | 269.5 | 38.6 | 131 | 22 | Human immune respo    |
| 21 | 264.5 | 37.9 | 212 | 20 | Secreted protein e    |
| 22 | 199.5 | 28.6 | 137 | 22 | Bovine mammary tis    |
| 23 | 199.5 | 28.6 | 141 | 17 | Human FKBP-13 Immu    |
| 24 | 197.5 | 28.3 | 99  | 13 | Bovine FKBP. Bos      |
| 25 | 197   | 28.2 | 143 | 13 | Human FKBP. Homo sapi |
| 26 | 190.5 | 27.3 | 434 | 21 | Human pancreatic c    |
| 27 | 190   | 27.2 | 366 | 21 | Human prostate can    |
| 28 | 190   | 27.2 | 582 | 21 | Hydrophobic domain    |
| 29 | 190   | 27.2 | 582 | 21 | Human isomerase ho    |
| 30 | 189   | 27.1 | 441 | 20 | Amino acid sequenc    |
| 31 | 187.5 | 26.9 | 388 | 20 | Amino acid sequenc    |
| 32 | 187.5 | 26.9 | 541 | 20 | Amino acid sequenc    |
| 33 | 187.5 | 26.9 | 570 | 22 | Amino acid sequenc    |
| 34 | 187   | 26.8 | 316 | 20 | Human membrane or     |
| 35 | 186.5 | 26.7 | 159 | 21 | Amino acid sequenc    |
| 36 | 186.5 | 26.7 | 163 | 21 | Arabidopsis thalia    |
| 37 | 178.5 | 25.6 | 146 | 21 | Arabidopsis thalia    |
| 38 | 178.5 | 25.6 | 152 | 21 | Arabidopsis thalia    |
| 39 | 178.5 | 25.6 | 153 | 21 | Arabidopsis thalia    |
| 40 | 176.5 | 25.3 | 146 | 21 | Arabidopsis thalia    |
| 41 | 176.5 | 25.3 | 152 | 21 | Arabidopsis thalia    |
| 42 | 176.5 | 25.3 | 153 | 21 | Arabidopsis thalia    |
| 43 | 163.5 | 23.4 | 201 | 21 | Human ORFX ORF2616    |
| 44 | 163.5 | 23.4 | 201 | 21 | Human PRO535 prote    |
| 45 | 163.5 | 23.4 | 201 | 21 | Human secreted pro    |

#### ALIGNMENTS

|          |  |                                     |
|----------|--|-------------------------------------|
| RESULT 1 | AAV32922   | AAV32922 standard; Protein: 129 AA. |
| ID       | AAV32922;  |                                     |
| AC       | AAV32922;  |                                     |
| XX       |  |                                     |
| DF       | 04-NOV-1999 (first entry)  |                                     |
| XX       |  |                                     |
| DE       | Transmembrane domain containing protein clone Hp01434.                 |                                     |
| XX       |  |                                     |
| KW       | Transmembrane domain containing protein; human; antibody production;   |                                     |
| KW       | interaction assay; diagnosis; nutritional activity; cytokine;          |                                     |
| KW       | cell proliferation; cell differentiation activity; immune stimulant;   |                                     |
| KW       | immune suppressant; haematopoiesis regulator; tissue growth activity;  |                                     |
| KW       | activin; inhibin activity; chemotaxis; chemokinesis; haemostasis;      |                                     |
| KW       | thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor; |                                     |
| KW       | tumour inhibitor.  |                                     |
| XX       |  |                                     |
| OS       | Homo sapiens.  |                                     |
| XX       |  |                                     |
| PN       | W09943802-A2.  |                                     |
| XX       |  |                                     |
| PD       | 02-SEP-1999.   |                                     |
| XX       |  |                                     |
| PF       | 25-FEB-1999; 99WO-JP00875.   |                                     |
| XX       |  |                                     |
| PR       | 27-FEB-1998; 98JP-0046607.   |                                     |
| XX       |  |                                     |
| PA       | (PROT-) PROTEGENE INC.   |                                     |
| PA       | (SAGA) SAGAMI CHEM RES CENT.   |                                     |
| XX       |  |                                     |
| PI       | Kato S, Kimura T, Nakamura N, Sekine S;                                |                                     |
| XX       |  |                                     |
| DR       | WPI, 1999-527617/44.   |                                     |

DR N-PSDB; AAZ11176, AAZ11183.

PT New proteins and DNA useful for preventing tumours

PS Claim 1; Page 70-71; 96pp; English.

CC This sentence is a human transmembrane protein of the invention. The  
CC DNAs are useful for expressing recombinant protein for analysts,  
CC characterisation or therapeutic use, and are useful as markers for  
CC tissues in which the corresponding protein is preferentially expressed.  
CC They are also useful as molecular weight markers on Southern gels, as  
CC chromosome markers or tags (when labelled) to identify potential genetic  
CC disorders, as probes to hybridise and thus discover novel, related DNA  
CC sequences, as a source of PCR primers for genetic fingerprinting, as  
CC probes to subtract-out known sequences in the process of discovering  
CC other novel DNAs, for selecting and making oligomers for attachment to a  
CC gene chip or other support, including for examination of expression  
CC patterns, to raise anti-protein antibodies using DNA immunisation  
CC techniques, and as an antigen to raise anti-DNA antibodies or elicit  
CC another immune response. Where the DNA encodes a protein which binds to  
CC another protein (e.g. in a receptor-ligand interaction), the DNA can also  
CC be used in interaction trap assays to identify DNAs encoding the other  
CC protein with which binding occurs or to identify inhibitors of the  
CC binding interaction. The DNAs and proteins can have e.g. nutritional  
CC activity, cytokine and cell proliferation/differentiation activity,  
CC immune stimulating (e.g. as vaccines) or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC activator/inhibitor activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity.

SQ Sequence 129 AA;

|                           |        |                    |           |             |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match               | 100.0% | Score 698:         | DB 20:    | length 129; |
| Best Local Similarity     | 100.0% | Pred. No. 1.1e-75: |           |             |
| Matches 129; Conservative | 0;     | Mismatches 0;      | Indels 0; | Gaps 0      |

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MHFLRRLVTFVFLMLDPTAORRKKKEESTEEVKKIVLHRLHPEKSSSTYSKSGDILNAAHYGL   | 50  |
|    |     | 1 mfflffrlfvyfwjlfcaqyqkkeesteekievlnhpencsktskkgdlnahdygl        | 60  |
| Db |     |   |     |
| QY | 61  | ARDGSKFCSFQNFONGHPKRWFLVAGVYITKGDIAMTMCGEKKRWVIPPSEAFYKREGY       | 120 |
| Db | 61  | akdgskfcsfcsftrngnqghpkrwflvlgvqylkgladlmtcmcpgekrkvvippsfaykyegy | 120 |
| QY | 121 | DKPLAKGI  | 129 |
|    |     |   |     |
| Db | 121 | dkpllakg1   | 129 |

|          |                                     |
|----------|-------------------------------------|
| RESULT   | 2                                   |
| AAW88556 |                                     |
| ID       | AAW88556 standard; Protein; 219 AA. |

AC AAW88556;

DT 01-MAR-1999 (first entry)

DE Secreted protein encoded by gene 23 clone HSQE084

KM Human; secreted protein; fusion protein; gene therapy; protein therapy  
KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia  
KM developmental abnormality; fetal deficiency; blood; allergy; renal;  
KM immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;  
KM inflammation; ischaemic shock; Alzheimer's disease; osteoclasts; AIDS  
KM cognitive disorder; schizophrenia; prostate; obesity; thymus  
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion  
KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm

OS Homo sapiens.

XX

PN W09854963-A2

PD 10-DEC-1998

PF 04-JUN-1998

98WO-US11422.

|    |             |              |
|----|-------------|--------------|
| PR | 18-DEC-1997 | 97US-0070923 |
| PR | 06-JUN-1997 | 97US-0048877 |
| PR | 06-JUN-1997 | 97US-0048881 |
| PR | 06-JUN-1997 | 97US-0048884 |
| PR | 06-JUN-1997 | 97US-0048893 |
| PR | 06-JUN-1997 | 97US-0048896 |
| PR | 06-JUN-1997 | 97US-0048899 |
| PR | 06-JUN-1997 | 97US-0048915 |
| PR | 06-JUN-1997 | 97US-0048949 |
| PR | 06-JUN-1997 | 97US-0048964 |
| PR | 06-JUN-1997 | 97US-0048972 |
| PR | 06-JUN-1997 | 97US-0049020 |
| PR | 06-JUN-1997 | 97US-0049375 |
| PR | 05-SEP-1997 | 97US-0056268 |
| PR | 05-SEP-1997 | 97US-0057635 |
| PR | 05-SEP-1997 | 97US-0057644 |
| PR | 05-SEP-1997 | 97US-0057647 |
| PR | 05-SEP-1997 | 97US-0057650 |
| PR | 05-SEP-1997 | 97US-0057661 |
| PR | 05-SEP-1997 | 97US-0057667 |
| PR | 05-SEP-1997 | 97US-0057761 |
| PR | 05-SEP-1997 | 97US-0057764 |
| PR | 05-SEP-1997 | 97US-0057770 |
| PR | 05-SEP-1997 | 97US-0057775 |
| PR | 05-SEP-1997 | 97US-0057778 |
| PR | 06-JUN-1997 | 97US-0048875 |
| PR | 06-JUN-1997 | 97US-0048878 |
| PR | 06-JUN-1997 | 97US-0048882 |
| PR | 06-JUN-1997 | 97US-0048884 |
| PR | 06-JUN-1997 | 97US-0048885 |
| PR | 06-JUN-1997 | 97US-0048900 |
| PR | 06-JUN-1997 | 97US-0048937 |
| PR | 06-JUN-1997 | 97US-0048916 |
| PR | 06-JUN-1997 | 97US-0048962 |
| PR | 06-JUN-1997 | 97US-0048974 |
| PR | 06-JUN-1997 | 97US-0049373 |
| PR | 05-SEP-1997 | 97US-0057529 |
| PR | 05-SEP-1997 | 97US-0057544 |
| PR | 05-SEP-1997 | 97US-0057642 |
| PR | 05-SEP-1997 | 97US-0057645 |
| PR | 05-SEP-1997 | 97US-0057648 |
| PR | 05-SEP-1997 | 97US-0057651 |
| PR | 05-SEP-1997 | 97US-0057662 |
| PR | 05-SEP-1997 | 97US-0057666 |
| PR | 05-SEP-1997 | 97US-0057755 |
| PR | 05-SEP-1997 | 97US-0057771 |
| PR | 05-SEP-1997 | 97US-0057776 |
| PR | 06-JUN-1997 | 97US-0048876 |
| PR | 06-JUN-1997 | 97US-0048880 |
| PR | 06-JUN-1997 | 97US-0048891 |
| PR | 06-JUN-1997 | 97US-0048913 |
| PR | 06-JUN-1997 | 97US-0048951 |
| PR | 06-JUN-1997 | 97US-0048954 |
| PR | 06-JUN-1997 | 97US-0057649 |
| PR | 05-SEP-1997 | 97US-0057654 |
| PR | 05-SEP-1997 | 97US-0057655 |

PR 05-SEP-1997; 97US-0057666.  
PR 05-SEP-1997; 97US-0057760.  
PR 05-SEP-1997; 97US-0057763.  
PR 05-SEP-1997; 97US-0057769.  
PR 05-SEP-1997; 97US-0057774.  
PR 05-SEP-1997; 97US-0057777.

(HUMA-) HUMAN GENOME SCI INC.

DR Brewster LA, Carter KC, Dillon PJ, Ebner R, Endress GA  
 PI Fan P, Feng P, Ferrite AM, Fischer CL, Florence C,  
 PI Florence K, Greene JM, Hu Z, Kyaw H, Lafleur DW,  
 PI Li Y, Moore PA, Ni Q, Olsen HS, Rosen CA, Ruben SM,  
 PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z,  
 XR  
 DR  
 WP1: 1999-059865/05.  
 DR  
 N-PSDB: AAV84433.

PT new isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX

PS Claim 11; Page 500-501; 772pp; English.  
XY

The invention relates to nucleic acid sequences (AA84411 to AA94633) encoding human secreted proteins (AA88534 to AA88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for art useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descriptor line for gene number and clone identification).

|          |        |
|----------|--------|
| Sequence | 219 AA |
|----------|--------|

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 93.68;          | Score 653;         | DB 20;    | Length 219; |
| Best Local Similarity | 100.08;         | Pred. No. 5,2e-70; |           |             |
| Matches 120;          | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0      |

|    |    |   |     |
|----|----|---|-----|
| 09 | 1  | MHFFRFVEFYVYLMGLTAAOROKKESTEEVKEVLEVLAHRENSKTSKSGKGLDLNHHGYGL | 60  |
| 10 | 1  | mhffrrfrrfvyfllmglftaqgrkkeesteevklevlhnrensktskskglldlnhgygl | 60  |
| 11 | 61 | AKDSKPFCSGSTONEGSHPRKEVLYGVGOVLKGDIAMTDMCPRKKNVYIPPSFAVGEQY   | 120 |
| 12 | 61 | akdskpfycsctltneghshprkfvlygvqvllkgldiamtcmprkknvlyppsfaygqey | 120 |

| RESULT   | 3                                  |
|----------|------------------------------------|
| AAB24429 |                                    |
| ID       | AAB24429 standard; Protein; 222 AA |
| XX       | XX                                 |
| AC       | AAB24429;                          |
| XX       |                                    |
| DT       | 07-NOV-2000 (first entry)          |

|    |  |
|----|--|
| XX |  |
| DE | Human PRO1304 protein sequence SEQ ID NO:205 |
| XX |  |

KM Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KM diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KM angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;  
KM cytosolic; gene therapy; vaccine

OS Homo sapiens.

PN WO200032221-A2.

PD 08-JUN-2000  
VY

PE 30-NOV-1999; 99WO-US28313.  
XX

|    |             |               |
|----|-------------|---------------|
| PR | 16-DEC-1958 | 98M0-05621508 |
| PR | 16-DEC-1958 | 98M0-05128510 |
| PR | 12-JAN-1959 | 99M0-01128550 |
| PR | 08-MAR-1959 | 99M0-01155544 |
| PR | 12-MAR-1959 | 99M0-05050528 |
| PR | 28-APR-1959 | 99M0-01233557 |
| PR | 14-MAY-1959 | 99M0-01314445 |
| PR | 02-JUN-1959 | 99M0-0134287  |
| PR | 23-JUN-1959 | 99M0-05112352 |
| PR | 20-JUL-1959 | 99M0-01410337 |
| PR | 26-JUL-1959 | 99M0-01447558 |
| PR | 01-SEP-1959 | 99M0-01456568 |
| PR | 08-SEP-1959 | 99M0-05620111 |
| PR | 13-SEP-1959 | 99M0-05205954 |
| PR | 15-SEP-1959 | 99M0-05209644 |
| PR | 15-SEP-1959 | 99M0-05210990 |
| PR | 05-OCT-1959 | 99M0-0521547  |
| PR | 29-OCT-1959 | 99M0-0523089  |
| PR |             | 99M0-01623062 |

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Garber H, Hillan KJ, Goddard A  
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V,  
PI Watanabe CK, Williams PM, Wood WI;

DR WPI; 2000-412154/35.  
DR N-PSDB; AAA77672.

PT Nucleic acids encoding PRO polypeptides useful for preventing, PT diagnosing and treating diagnosing a cardiovascular, endothelial or PT angiogenic disorders in mammals -

PS Claim 72; Fig 84; 315pp; English.

The present invention describes nucleic acids encoding PRO polypeptide useful for preventing, diagnosing and treating disorders of cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA7510 to AAA77721 and AAB24386 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.

Sequence . 222 AA;

|                           |         |                    |        |                  |
|---------------------------|---------|--------------------|--------|------------------|
| Query Match               | 93.6%;  | Score 653;         | DB 21; | Length 222;      |
| Best Local Similarity     | 100.0%; | Pred. No. 5.3e-70; |        |                  |
| Matches 120; Conservative | 0;      | Mismatches         | 0;     | Indels 0; Gaps 0 |

0Y 1 MHFLFRIVFFYLWGLTTAQRÖKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDYL 600

Db 5 mbllflfivfiyfwlftqgrqkkesteevkvlethrpenscktskkgdlnahydyj 64  
QY 61 AKDGSKFYCSFRONESHHPKWFVLGVCQVTKGDIANTDMCPGKRRVVPSPFAFGKEGY 120  
Db 65 akdgskfycsrtneghphkfwfivgvgvikjldiantdmcpkrrkvlpfpfaygkey 124

RESULT 4  
ID AAY99391 standard; Protein; 222 AA.  
AC AAY99391;  
XX  
XX 08-AUG-2000 (first entry)  
DT Human PRO1304 (UN0670) amino acid sequence SEQ ID NO:180.  
DE Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
XX Homo sapiens.  
XX MO200012708-A2.  
PN 09-MAR-2000.  
PD 01-SEP-1999; 99MO-US02111.  
XX 01-SEP-1998; 98US-0098716.  
PR 01-SEP-1998; 98US-0098749.  
PR 01-SEP-1998; 98US-0098803.  
PR 02-SEP-1998; 98US-0098821.  
PR 02-SEP-1998; 98US-0098843.  
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PR 09-SEP-1998; 98US-0099596.  
PR 09-SEP-1998; 98US-0099598.  
PR 09-SEP-1998; 98US-0099602.  
PR 09-SEP-1998; 98US-0099642.  
PR 10-SEP-1998; 98US-0099741.  
PR 10-SEP-1998; 98US-0099754.  
PR 10-SEP-1998; 98US-0099763.  
PR 10-SEP-1998; 98US-0099792.  
PR 10-SEP-1998; 98US-0099808.  
PR 10-SEP-1998; 98US-0099812.  
PR 10-SEP-1998; 98US-0099815.  
PR 15-SEP-1998; 98US-0099816.  
PR 15-SEP-1998; 98US-0100385.  
PR 15-SEP-1998; 98US-0100388.  
PR 15-SEP-1998; 98US-0100390.  
PR 16-SEP-1998; 98US-0100584.  
PR 16-SEP-1998; 98US-0100627.  
PR 16-SEP-1998; 98US-0100661.  
PR 16-SEP-1998; 98US-0100664.  
PR 16-SEP-1998; 98US-0100664.  
PR 17-SEP-1998; 98US-0100683.  
PR 17-SEP-1998; 98US-0100684.  
PR 17-SEP-1998; 98US-0100710.  
PR 17-SEP-1998; 98US-0100711.  
PR 17-SEP-1998; 98US-0100919.  
PR 17-SEP-1998; 98US-0100930.  
PR 18-SEP-1998; 98US-0100930.  
PR 18-SEP-1998; 98US-0100848.  
PR 18-SEP-1998; 98US-0100849.  
PR 18-SEP-1998; 98US-0101014.  
PR 18-SEP-1998; 98US-0101068.  
PR 18-SEP-1998; 98US-0101071.  
PR 22-SEP-1998; 98US-0101279.  
PR 23-SEP-1998; 98US-0101471.  
PR 23-SEP-1998; 98US-0101471.  
PR 23-SEP-1998; 98US-0101474.  
PR 23-SEP-1998; 98US-0101475.  
PR 23-SEP-1998; 98US-0101476.

PR 23-SEP-1998; 98US-0101477.  
PR 23-SEP-1998; 98US-0101479.  
PR 24-SEP-1998; 98US-0101741.  
PR 24-SEP-1998; 98US-0101741.  
PR 24-SEP-1998; 98US-0101743.  
PR 24-SEP-1998; 98US-0101915.  
PR 24-SEP-1998; 98US-0101916.  
PR 29-SEP-1998; 98US-0102207.  
PR 29-SEP-1998; 98US-0102240.  
PR 29-SEP-1998; 98US-0102307.  
PR 29-SEP-1998; 98US-0102330.  
PR 29-SEP-1998; 98US-0102331.  
PR 30-SEP-1998; 98US-0102484.  
PR 30-SEP-1998; 98US-0102487.  
PR 30-SEP-1998; 98US-0102547.  
PR 30-SEP-1998; 98US-0102571.  
PR 30-SEP-1998; 98US-0102571.  
PR 01-OCT-1998; 98US-0102684.  
PR 01-OCT-1998; 98US-0102687.  
PR 02-OCT-1998; 98US-0102965.  
PR 06-OCT-1998; 98US-0103258.  
PR 06-OCT-1998; 98US-0103449.  
PR 07-OCT-1998; 98US-0103314.  
PR 07-OCT-1998; 98US-0103315.  
PR 07-OCT-1998; 98US-0103315.  
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PR 07-OCT-1998; 98US-0103395.  
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PR 08-OCT-1998; 98US-0103633.  
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PR 08-OCT-1998; 98US-0103679.  
PR 08-OCT-1998; 98US-0103711.  
PR 14-OCT-1998; 98US-0104257.  
PR 20-OCT-1998; 98US-0104987.  
PR 20-OCT-1998; 98US-0105000.  
PR 20-OCT-1998; 98US-0105002.  
PR 21-OCT-1998; 98US-0105104.  
PR 22-OCT-1998; 98US-0105169.  
PR 22-OCT-1998; 98US-0105266.  
PR 26-OCT-1998; 98US-0105693.  
PR 26-OCT-1998; 98US-0105694.  
PR 27-OCT-1998; 98US-0105807.  
PR 27-OCT-1998; 98US-0105881.  
PR 27-OCT-1998; 98US-0105882.  
PR 27-OCT-1998; 98US-0106062.  
PR 28-OCT-1998; 98US-0106023.  
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PR 28-OCT-1998; 98US-0106030.  
PR 28-OCT-1998; 98US-0106032.  
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PR 29-OCT-1998; 98US-0106248.  
PR 29-OCT-1998; 98US-0106384.  
PR 29-OCT-1998; 98US-0106500.  
PR 30-OCT-1998; 98US-0106464.  
PR 03-NOV-1998; 98US-0106856.  
PR 03-NOV-1998; 98US-0106902.  
PR 03-NOV-1998; 98US-0106905.  
PR 03-NOV-1998; 98US-0106919.  
PR 03-NOV-1998; 98US-0106932.  
PR 10-NOV-1998; 98US-0106934.  
PR 10-NOV-1998; 98US-0107783.  
PR 17-NOV-1998; 98US-0108775.  
PR 17-NOV-1998; 98US-0108779.  
PR 17-NOV-1998; 98US-0108787.  
PR 17-NOV-1998; 98US-0108788.  
PR 17-NOV-1998; 98US-0108801.  
PR 17-NOV-1998; 98US-0108802.  
PR 17-NOV-1998; 98US-0108806.  
PR 17-NOV-1998; 98US-0108807.  
PR 17-NOV-1998; 98US-0108867.  
PR 17-NOV-1998; 98US-0108925.  
PR 18-NOV-1998; 98US-0108848.  
PR 18-NOV-1998; 98US-0108849.

PR 18-NOV-1998; 98US-0108650.  
 PR 18-NOV-1998; 98US-0108651.  
 PR 18-NOV-1998; 98US-0108652.  
 PR 18-NOV-1998; 98US-0108658.  
 PR 18-NOV-1998; 98US-0108904.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI.  
 DR N-PSDB; AAA37073.  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or  
 PT secreted PRO polypeptides, useful for screening of potential peptide or  
 PT small molecule inhibitors of the relevant receptor/ligand interactions  
 XX  
 PS Claim 12; Fig 104; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent  
 CC PCR primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention.  
 XX

SO Sequence 222 AA;

Query Match 93.6%; Score 653; DB 21; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-70;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLRFVFEFLMGFTLQROKKESTEVEKIEVLAHPENCSTSKKGDLLNAHYDGL 60  
 Db 5 mHlflrfvfyflwglftqqrqkkeestevekvlelhrencsktskkgd1lnahydy1 64  
 OY 61 AKDSEKFCSTRTONGHPRKFWVLGVGVYIKGLDIAMTDMCPGEEKRVYIPSPFAYGREGY 120  
 Db 65 akdskfcstrtonghprkfwvlgvgyikgldiamtdmcpgekrkvvippsfaygkey 124

RESULT 5

AAB66140 ID AAB66140 standard; protein; 222 AA.

AC AAB66140;

DT 02-APR-2001 (first entry)

XX Protein of the invention #52.

KW Secreted; transmembrane; gene therapy.

OS Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000WO-US04342.

XX 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99US-0162506.

PR 02-DEC-1999; 99US-0162506.

PR 16-DEC-1999; 99US-0162506.

PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 XX

PA (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX

DR WPI: 2001-071395/08.

XX  
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy -  
 XX

PS Claim 1; Fig 104; 787pp; English.

CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of  
 CC anti-sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents.  
 CC The nucleic acids may also be used in gene therapy.  
 XX

SO Sequence 222 AA;

Query Match 93.6%; Score 653; DB 22; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-70;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLRFVFEFLMGFTLQROKKESTEVEKIEVLAHPENCSTSKKGDLLNAHYDGL 60  
 Db 5 mHlflrfvfyflwglftqqrqkkeestevekvlelhrencsktskkgd1lnahydy1 64  
 OY 61 AKDSEKFCSTRTONGHPRKFWVLGVGVYIKGLDIAMTDMCPGEEKRVYIPSPFAYGREGY 120  
 Db 65 akdskfcstrtonghprkfwvlgvgyikgldiamtdmcpgekrkvvippsfaygkey 124

RESULT 6

AAB50988 ID AAB50988 standard; protein; 222 AA.

AC AAB50988;

DT 21-MAR-2001 (first entry)

XX Human PRO1304 protein.

DE Human PRO1304 protein.

XX Human: PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotrophic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
 KW vunerary; antiangioma; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 KW wound healing.  
 XX

OS Homo sapiens.

PN WO200073445-A2.

PD 07-DEC-2000.

PF 17-MAY-2000; 2000WO-US13705.

XX 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99US-0146222.

PR 30-NOV-1999; 99WO-US28313.



PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertlisen ME,  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA,  
 PI Pooni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI:

DR WPI; 2001-025251/03.  
 DR N-PSDB; AAC90572.

PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -

XX Claim 71; Fig 20; 182pp; English.

XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC stenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.

XX Sequence 222 AA;

Query Match 93.6%; Score 653; DB 22; Length 222;

Best Local Similarity 100.0%; Pred. No. 5.3e-70; Mismatches 0; Indels 0; Gaps 0;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLFRFVFFYLMGLFTAOROKKEESTEVKIEVLHHPENCSTKSKGDLNAHYDYL 60  
 DB 5 mhflfrfivffylwglftagrqkkeeestevkievlhnpencstkskkgdlinahydyl 64  
 OY 61 AKDGSKFYCSRTQNEGHKRWFLVGVGVYIKGLDIAMTDMCGEKKRWVIRPSFAVGEKGY 120  
 DB 65 akdgskfycsrtqneghkfwlvgvgyikgldiamtcmcpgekkrvvipsfaygkgy 124

RESULT 7

AAV84868  
 ID AAV84868 standard; Protein: 222 AA.

AC AAV84868;

DT 08-AUG-2000 (first entry)

XX Amino acid sequence of a human FK506 binding protein (FKBP).

XX Human; FK506 binding protein; FKBP; NPAAEB04; cancer; diabetes mellitus;

XX kidney disease; autoimmune disease; metabolic disorder; vaccine;

XX gene therapy.

XX Homo sapiens.

XX OS

XX

PN WO200021992-A1.

XX 20-APR-2000.

XX 09-OCT-1998; 98WO-CN00220.

XX 09-OCT-1998; 98WO-CN00220.

XX (UYSH-) UNIV SHANGHAI SECOND MEDICAL.

XX Song H, Han Z, Hu R, Huang C, Ren S;

XX WPI; 2000-317939/27.

XX N-PSDB; AAA14950.

XX New polypeptide designated NPAAEB04 useful for diagnosing and treating  
 XX cancer and diabetes is thought to be FKBP5 binding protein -  
 XX Claim 1; Page 20; 32pp; English.

XX The present sequence represents a human FK506 binding protein (FKBP),  
 CC designated NPAAEB04. The protein may be used to screen for its agonists  
 CC and antagonists. Diseases or conditions arising from altered expression  
 CC or activity of NPAAEB04 may be diagnosed by detecting NPAAEB04 in a  
 CC sample from a patient or detecting a mutation in the NPAAEB04 gene in  
 CC the genome of a patient. These diseases or conditions include cancer,  
 CC diabetes mellitus, kidney disease, autoimmune diseases or metabolic  
 CC disorders. The FKBP polynucleotides and polypeptides may be administered  
 CC to patients as vaccines or as part of a gene therapy regime.  
 CC respectively, to treat these diseases or conditions.

XX Sequence 222 AA;

Query Match 92.8%; Score 648; DB 21; Length 222;

Best Local Similarity 99.2%; Pred. No. 2.1e-69; Mismatches 0; Indels 0; Gaps 0;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLFRFVFFYLMGLFTAOROKKEESTEVKIEVLHHPENCSTKSKGDLNAHYDYL 60  
 DB 5 mhflfrfivffylwglftagrqkkeeestevkievlhnpencstkskkgdlinahydyl 64  
 OY 61 AKDGSKFYCSRTQNEGHKRWFLVGVGVYIKGLDIAMTDMCGEKKRWVIRPSFAVGEKGY 120  
 DB 65 akdgskfycsrtqneghkfwlvgvgyikgldiamtcmcpgekkrvvipsfaygkgy 124

RESULT 8

AAV65390  
 ID AAV65390 standard; Protein: 68 AA.

AC AAV65390;

DT 01-FEB-2000 (first entry)

XX Human 5' EST related polypeptide SEQ ID NO:1551.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;

XX gene therapy; chromosome mapping; upstream regulatory sequence;

XX forensic; location; development; protein synthesis; stability;

XX regulation; identification.

XX Homo sapiens.

XX OS

XX

XX

XX

PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-038446/03.  
 DR N-PSDB: AA243004.  
 XX  
 PT Novel secreted protein 5' expressed sequence tag sequences used in  
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures  
 XX  
 PS Claim 3; Page 817; 837pp; English.  
 XX  
 CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)  
 CC sequences, corresponding to human secreted proteins. AA242265 to  
 CC AA243075 represent the EST-related proteins corresponding to AA242265 to  
 CC AA243075. The 5' ESTs can be used for producing secreted human gene  
 CC products. They can be used to identify and isolate 5' untranslated  
 CC regions (UTRs) and upstream regulatory regions which control the  
 CC location, development stage, rate, and quantity of protein synthesis, as  
 CC well as stability of mRNA. The ESTs are also useful as probes for  
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can  
 CC also be used in forensic procedures to identify individuals, or in  
 CC diagnostic procedures to identify individuals having genetic diseases  
 CC resulting from abnormal gene expression. The products may also be used in  
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be  
 CC used for directing extracellular secretion of a polypeptide or the  
 CC insertion of a polypeptide into a membrane, or importing a polypeptide  
 CC into a cell. The proteins encoded by the EST sequences may be useful in  
 CC treating a variety of human conditions. Secreted proteins have  
 CC therapeutic value, and the identification of new secreted proteins is  
 CC valuable. AA242249 to AA242264 and AA242264 to AA242265 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 68 AA:  
 Query Match 49.3%; Score 344; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred No. 9.8e-34;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHFLRFIVEFYLMGLTAAQRORKEESTETEVLRHPENCSTKSKGDLNAHYDGYL 60  
 Db |||||  
 5 mhflrfivfywglftagrqrkkestevklevlhrpencsktskkgdlnahdygl 64  
 QY 61 AKDG 64  
 Db ||||  
 65 akdg 68  
 Db 65 akdg 68  
 RESULT 9  
 AA088744  
 ID AA088744 standard; Protein; 57 AA.  
 XX  
 AC AA088744;  
 XX  
 DT 01-MAR-1999 (first entry)  
 XX  
 DE Secreted protein encoded by gene 23 clone HSOE084.  
 XX  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KW immune system; ischaemic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9854963-A2.  
 XX  
 PD 10-DEC-1998.

XX  
 PF 04-JUN-1998; 98WO-US11422.  
 XX  
 PR 18-DEC-1997; 97US-0070923.  
 PR 06-JUN-1997; 97US-0048877.  
 PR 06-JUN-1997; 97US-0048881.  
 PR 06-JUN-1997; 97US-0048884.  
 PR 06-JUN-1997; 97US-0048893.  
 PR 06-JUN-1997; 97US-0048896.  
 PR 06-JUN-1997; 97US-0048899.  
 PR 06-JUN-1997; 97US-0048915.  
 PR 06-JUN-1997; 97US-0048949.  
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 PR 06-JUN-1997; 97US-0049020.  
 PR 05-SEP-1997; 97US-0049375.  
 PR 05-SEP-1997; 97US-0057628.  
 PR 05-SEP-1997; 97US-0057635.  
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 PR 05-SEP-1997; 97US-0057647.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057651.  
 PR 05-SEP-1997; 97US-0057661.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 05-SEP-1997; 97US-0057764.  
 PR 05-SEP-1997; 97US-0057770.  
 PR 05-SEP-1997; 97US-0057775.  
 PR 05-SEP-1997; 97US-0057778.  
 PR 06-JUN-1997; 97US-0048875.  
 PR 06-JUN-1997; 97US-0048878.  
 PR 06-JUN-1997; 97US-0048882.  
 PR 06-JUN-1997; 97US-0048885.  
 PR 06-JUN-1997; 97US-0048894.  
 PR 06-JUN-1997; 97US-0048897.  
 PR 06-JUN-1997; 97US-0048900.  
 PR 06-JUN-1997; 97US-0048916.  
 PR 06-JUN-1997; 97US-0048962.  
 PR 06-JUN-1997; 97US-0048970.  
 PR 06-JUN-1997; 97US-0048974.  
 PR 05-SEP-1997; 97US-0049373.  
 PR 05-SEP-1997; 97US-0057629.  
 PR 05-SEP-1997; 97US-0057642.  
 PR 05-SEP-1997; 97US-0057645.  
 PR 05-SEP-1997; 97US-0057648.  
 PR 05-SEP-1997; 97US-0057651.  
 PR 05-SEP-1997; 97US-0057662.  
 PR 05-SEP-1997; 97US-0057668.  
 PR 05-SEP-1997; 97US-0057762.  
 PR 05-SEP-1997; 97US-0057765.  
 PR 05-SEP-1997; 97US-0057771.  
 PR 05-SEP-1997; 97US-0057776.  
 PR 06-JUN-1997; 97US-0048876.  
 PR 06-JUN-1997; 97US-0048880.  
 PR 06-JUN-1997; 97US-0048883.  
 PR 06-JUN-1997; 97US-0048892.  
 PR 06-JUN-1997; 97US-0048895.  
 PR 06-JUN-1997; 97US-0048898.  
 PR 06-JUN-1997; 97US-0048901.  
 PR 06-JUN-1997; 97US-0048917.  
 PR 06-JUN-1997; 97US-0048963.  
 PR 06-JUN-1997; 97US-0048971.  
 PR 06-JUN-1997; 97US-0049019.  
 PR 06-JUN-1997; 97US-0049374.  
 PR 05-SEP-1997; 97US-0057627.  
 PR 05-SEP-1997; 97US-0057634.  
 PR 05-SEP-1997; 97US-0057643.  
 PR 05-SEP-1997; 97US-0057646.  
 PR 05-SEP-1997; 97US-0057649.  
 PR 05-SEP-1997; 97US-0057654.  
 PR 05-SEP-1997; 97US-0057666.  
 PR 05-SEP-1997; 97US-0057760.  
 PR 05-SEP-1997; 97US-0057763.



PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085689.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.

(GETH ) GENENTECH INC.

XX PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX PI WPI: 1999-551358/46.  
 XX DR N-PSDB; AAX34013.

PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 XX adhesion disorders -

PS Claim 12; Fig 53; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AAX33891 to  
 CC AAX24338, and AAY1465 to AAY1774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX Sequence 211 AA;

Query Match 38.9%; Score 271.5; DB 20; Length 211;  
 Best Local Similarity 44.2%; Pred. No. 2.1e-24;  
 Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

OY 3 FLFRIVFVYLMGLTAAQROKKESTEVKTEVLRHPENCSTKSGLLLAHYGYLAK 62  
 || : : : | | : ||||| : | : : ||| : ||||| :  
 Db 4 flmaavlltflvslgslalpe-----pevklevlqkplchtktgqdlmlyvhyegylek 58  
 OY 63 DSKRFYCGRTONEGHPKRVVLGVGVINGLPIAMTDMCGEKRKRVVIPPSPAYGEGYDK 122  
 || : : : | | : ||||| : | : : ||| : ||||| : ||||| :  
 Db 59 dgsifshchkhngqpilwflgtlglealkywdqgklgmvcgckrllilppalgygkegkqk 118

RESULT 11

AAV01458

AC AAY01458;

XX 18-MAY-1999 (first entry)  
 XX

DE Polypeptide fragment encoded by gene 19.

XX Human, secreted protein; gene therapy; protein therapy; cancer; weight;  
 KW tumour; chromosome mapping; forensic; hematological disease; allergy;  
 KW inflammation; cell proliferation; viral infection; wound healing;  
 KW modulation; appetite; behaviour; food additive; preservative.

OS Homo sapiens.

PN WO9903990-A1.

XX 28-JAN-1999.

XX 15-JUL-1998; 98WO-US14613.

PR 18-AUG-1997; 97US-0056361.  
 PR 16-JUL-1997; 97US-0052661.  
 PR 16-JUL-1997; 97US-0052870.  
 PR 16-JUL-1997; 97US-0052871.  
 PR 16-JUL-1997; 97US-0052872.  
 PR 16-JUL-1997; 97US-0052873.  
 PR 16-JUL-1997; 97US-0052874.  
 PR 16-JUL-1997; 97US-0052875.  
 PR 22-JUL-1997; 97US-0053440.  
 PR 22-JUL-1997; 97US-0053441.  
 PR 22-JUL-1997; 97US-0053442.  
 PR 18-AUG-1997; 97US-0055683.  
 PR 18-AUG-1997; 97US-0055724.  
 PR 18-AUG-1997; 97US-0055725.  
 PR 18-AUG-1997; 97US-0055726.  
 PR 18-AUG-1997; 97US-0055727.  
 PR 18-AUG-1997; 97US-0055946.  
 PR 18-AUG-1997; 97US-0055952.  
 PR 18-AUG-1997; 97US-0055985.  
 PR 18-AUG-1997; 97US-0055989.  
 PR 18-AUG-1997; 97US-0056359.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Duan R, Feng P, Ferrle AM, Florence KA, Fouad J;  
 PI Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;  
 PI Yu G;

XX WPI: 1999-132234/11.  
 XX N-PSDB; AAX22229.

XX New nucleic acids encoding secreted human proteins - potentially  
 PT useful for treating and diagnosing diseases and identifying specific  
 PT binding agents

XX Disclosure; Page 21; 251pp; English.

XX The invention relates to nucleic acid sequences (AAX22211 to AAX22282)  
 CC encoding human secreted proteins (AAY01383 to AAY01454). The secreted  
 CC protein gene sequences are deposited with the ATCC under deposit number  
 CC ATCC 209138, 209139 or 209141. Host cells containing vectors comprising  
 CC the nucleic acid sequences are used for the recombinant expression of  
 CC the secreted proteins. The polynucleotide and amino acid sequences are  
 CC useful for preventing, treating or ameliorating medical conditions e.g.  
 CC by protein or gene therapy. Pathological conditions can be also diagnosed  
 CC by determining the amount of the new polypeptides in a sample or by the  
 CC presence of mutations in the new polynucleotides. The nucleic acid  
 CC sequences, or its fragments, are useful for chromosome identification  
 CC and mapping; as antisense and triplex-forming therapeutics; in gene  
 CC therapy; for (forensic) identification of individuals; as molecular  
 CC weight markers; to identify related sequences or specific mRNA; in  
 CC preparation of oligomers and to raise anti-DNA antibodies. Antibodies are  
 CC useful as immunoassay reagents (including for in vivo imaging) and  
 CC therapeutically to inhibit or activate particular polypeptides. A very  
 CC wide range of disorders may be treated with the polynucleotide and  
 CC polypeptide sequences, e.g. autoimmune or hematological diseases,  
 CC allergy, inflammation, cancer or other forms of cell proliferation, viral  
 CC or other infections. The sequences may also be useful in wound healing,  
 CC to modulate differentiation of embryonic stem cells, to modulate weight,

CC appetite, behaviour etc. and as food additive or preservative. The  
CC present sequence represents a polypeptide fragment encoded by a gene  
CC of the invention (see descriptor line for gene number).

XX Sequence 211 AA.

Query Match 38.9%; Score 271.5; DB 20; Length 211;

Best Local Similarity 44.2%; Pred. No. 2,1e-24;

Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

CC 3 FLFRFVFFYLMGLFTAAQRKKESTEEVKIEVLHREPCSKTSKKGDLNHHYDGLAK 62

CC 4 FLNVAVLITFVLSIGALIP-----PEVKLEVLKPKFICHTKTKYGGDLMVHYGYLEK 58

CC 63 DGSKFYCSRTQNGHPKPFVILGVGVKIGDIAMTDMPGKRRKRVIPSPFAYGKEGYDK 122

CC 59 dgsflfsthkhngpivftlgilalealkgwqgllkgmcvgekrklllppalgygkegkx 118

Db 59 dgsflfsthkhngpivftlgilalealkgwqgllkgmcvgekrklllppalgygkegkx 118

RESULT 12

ID AAB44262 standard; Protein; 211 AA.

XX AAB44262;

AC 08-FEB-2001 (first entry)

DE Human PRO381 (UNQ322) protein sequence SEQ ID NO:145.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;

XX expressed sequence tag; detection; cancer.

XX Homo sapiens.

XX WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000MO-US04341.

XX 08-MAR-1999; 99MO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 26-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130332.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99MO-US28313.

PR 02-DEC-1999; 99MO-US28551.

PR 16-DEC-1999; 99MO-US28565.

PR 30-DEC-1999; 99MO-US310095.

PR 30-DEC-1999; 99MO-US31274.

PR 05-JAN-2000; 2000MO-US00219.

PR 06-JAN-2000; 2000MO-US00276.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Geber H, Gerltzen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Kijavain IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

XX WPI: 2000-611443/58.

XX N-PSDB: AAC78488.

XX Novel PRO polypeptides and polynucleotides used in detection methods,

PT to target bioactive molecules to specific cells, and to modulate

PT cellular activities :

XX Claim 12; Fig 53; 636pp; English.

PS AAC78458 to AAC78599 represent polynucleotide and EST (expressed

CC sequence tag) sequences which encode secreted or transmembrane PRO

CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic

CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive

CC molecules to cells and for modulating biological activities of cells,

CC using the polypeptides for specific targeting. The polypeptide targeting

CC can be used to kill the target cells, e.g. for the treatment of cancers.

CC The polypeptide pairs provide specific targeting of bioactive molecules

CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in

CC the isolation of the PRO polynucleotide sequences.

XX Sequence 211 AA;

Query Match 38.9%; Score 271.5; DB 21; Length 211;

Best Local Similarity 44.2%; Pred. No. 2,1e-24;

Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

CC 3 FLFRFVFFYLMGLFTAAQRKKESTEEVKIEVLHREPCSKTSKKGDLNHHYDGLAK 62

CC 4 FLNVAVLITFVLSIGALIP-----PEVKLEVLKPKFICHTKTKYGGDLMVHYGYLEK 58

CC 63 DGSKFYCSRTQNGHPKPFVILGVGVKIGDIAMTDMPGKRRKRVIPSPFAYGKEGYDK 122

CC 59 dgsflfsthkhngpivftlgilalealkgwqgllkgmcvgekrklllppalgygkegkx 118

Db 59 dgsflfsthkhngpivftlgilalealkgwqgllkgmcvgekrklllppalgygkegkx 118

RESULT 13

ID AAB24021 standard; Protein; 211 AA.

XX AAB24021;

AC 25-JAN-2001 (first entry)

DE Human PRO381 protein sequence SEQ ID NO:2.

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;

XX identification; tumorigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200053750-A1.

PD 14-SEP-2000.

PF 02-DEC-1999; 99MO-US28551.

XX 08-MAR-1999; 99MO-US05028.

PR 01-SEP-1999; 99MO-US20111.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99MO-US28313.

PR 01-DEC-1999; 99MO-US28634.

XX (GETH ) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

PI WPI: 2000-594320/56.

DR N-PSDB: AAC58103.

XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit

PT the growth of tumors in mammals, and to identify inhibitors of PRO

PT polypeptide activity or expression -

XX Claim 61; Fig 2; 226pp; English.

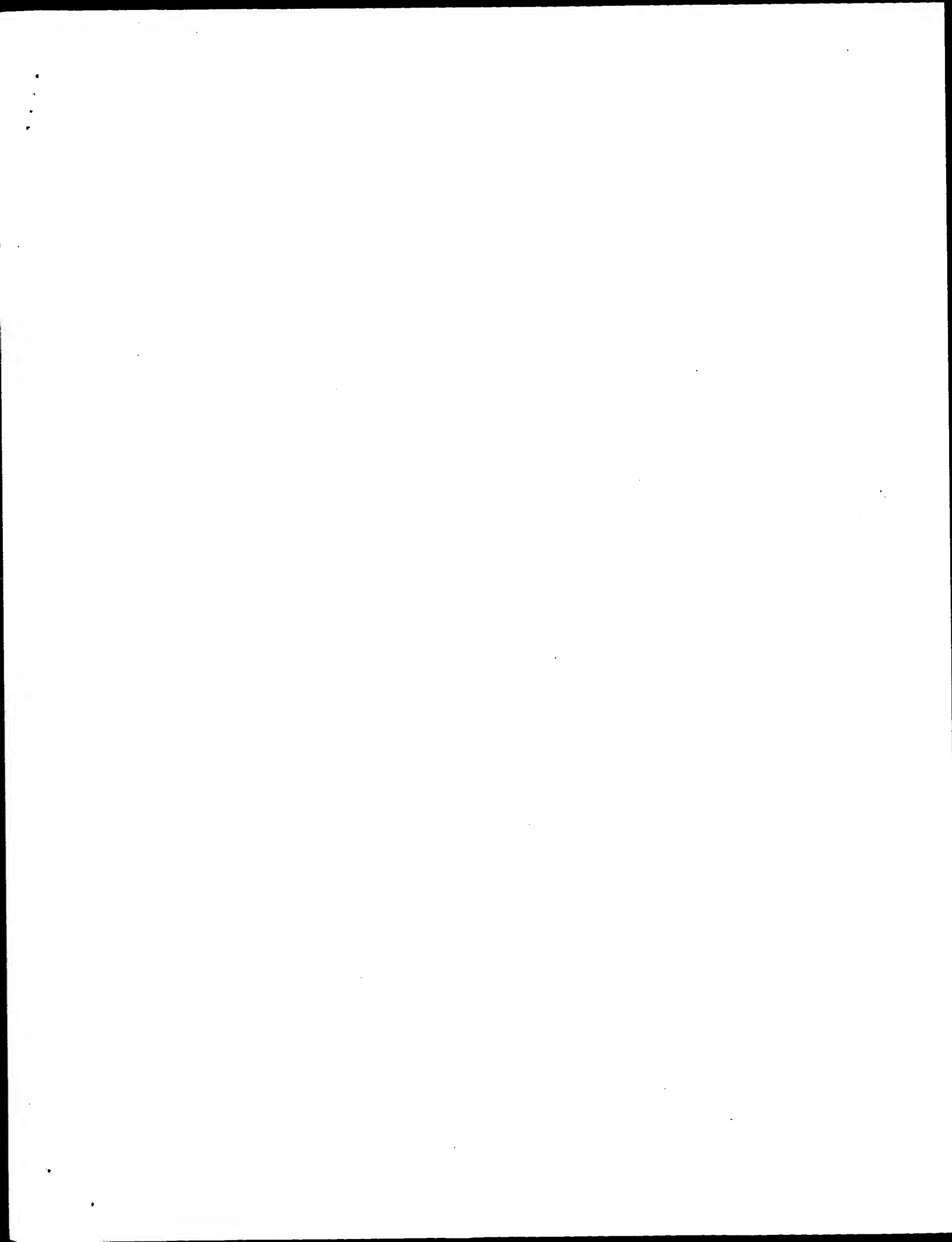
XX The present invention describes an antibody that binds to a human











QY 26 ESTEEVKIEVLHRPENCSTSKKGDLLNAHYDGYLAKDGSKFYCSRTQNEGHPKWFVLGV 85



```

US-08-989-386-1
Sequence 1, Application US/08989386
Patent No. 5989860
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSoft for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0443 US

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RESULT      6
US-08-899-6
: Sequence 6, Application us/08803899
: Patent No. 5912224
:
GENERAL INFORMATION:
APPLICANT: DONAHOE, PATRICIA K.
APPLICANT: WANG, TONGWEN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
CELLULAR RESPONSE TO TGF-BETA LIGANDS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STRENE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,899
FILING DATE: 02/21/1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/012,054
FILING DATE: 02/22/1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609,4240001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

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1 APPLICANT: Harding, Matthew W.
2 APPLICANT: Livingston, David J.
3 TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
4 TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
5 TITLE OF INVENTION: GNA
6 NUMBER OF SEQUENCES: 32
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
9 STREET: Two Militia Drive
10 CITY: Lexington
11 STATE: Massachusetts
12 COUNTRY: U.S.A.
13 ZIP: 02173
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/336,618
21 FILING DATE: 09-NOV-1994
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 07/963,325
25 FILING DATE: 16-OCT-1992
26 APPLICATION NUMBER: US 07/777,752
27 FILING DATE: 11-OCT-1991
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PC7/
30 FILING DATE: 09-OCT-1992
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Granahan, Patricia
33 REGISTRATION NUMBER: 32,227
34 REFERENCE/DOCKET NUMBER: VP191-06A
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 617-861-6240
37 TELEFAX: 617-861-9540
38 INFORMATION FOR SEQ ID NO: 19:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 88 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
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Query Match      23.4%; Score 163.5; DB 1; Length 88;
Best Local Similarity 42.6%; Pred. No. 1e-12;
Matches 40; Conservative 14; Mismatches 27; Indels 13; Gaps 3.

QY      26 ESTEEVAKIEVLRHPENCSTKSKGDLNAAHYDGYLAKDGSKFYCSRTQNGCHKPFWVLGY 85
      |:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      4 EGKRKLIGYKKRVDPHCPIKSKRGDVLNMYHTGKRL-EDGTFPDSLLPQNG--PFWSLGT 60
      |:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

QY      86 GQYIKGLDIAMDMDCEGKKRVVIPPSPAYGKG 119
      |:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      61 GQYIK-----EGEKRLVIPSSELGYGEG 84
      |:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 12
US-08-894-173-86
; Sequence 86, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
LENGTH: 104

```



Fri Aug 31 12:10:24 2001

us-09-622-522-1.ra1

Page 6

TYPE: PRT  
ORGANISM: Yeast  
US-08-894-173-86

Query Match 22.6%; Score 157.5; DB 3; Length 104;  
Best Local Similarity 45.0%; Pred. No. 7.1e-12;  
Matches 36; Conservative 11; Mismatches 30; Indels 3; Gaps 2;

QY 40 ENCSTKSGDILNAHYDGLAKDSKFCSTONEGHPKFWLVGQVITKIDIAMTDM 99  
DB 7 EDCLIMPGDKVKVHTGSL-ESGTVF--DSSYRSGSPIAFELGVRVIGKMDQVAGM 63

QY 100 CPGEKRVVIPPSPFAYGKEG 119  
DB 64 CVGEKRLQIPSSLAYGERG 83

RESULT 13  
US-09-398-193-86  
Sequence 86, Application US/09398193  
Patent No. 6197581  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
TITLE OF INVENTION: Adenylate cyclase and uses therefor  
FILE REFERENCE: P24360  
CURRENT APPLICATION NUMBER: US/09/398,193  
CURRENT FILING DATE: 1999-09-17  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 86  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Yeast  
US-09-398-193-86

Query Match 22.6%; Score 157.5; DB 4; Length 104;  
Best Local Similarity 45.0%; Pred. No. 7.1e-12;  
Matches 36; Conservative 11; Mismatches 30; Indels 3; Gaps 2;

QY 40 ENCSTKSGDILNAHYDGLAKDSKFCSTONEGHPKFWLVGQVITKIDIAMTDM 99  
DB 7 EDCLIMPGDKVKVHTGSL-ESGTVF--DSSYRSGSPIAFELGVRVIGKMDQVAGM 63

QY 100 CPGEKRVVIPPSPFAYGKEG 119  
DB 64 CVGEKRLQIPSSLAYGERG 83

RESULT 14  
US-08-894-173-66  
Sequence 66, Application US/08894173A  
Patent No. 6090612  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
TITLE OF INVENTION: Adenylate cyclase and uses therefor  
FILE REFERENCE: P14716C  
CURRENT APPLICATION NUMBER: US/08/894,173A  
CURRENT FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 66  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-08-894-173-66

Query Match 20.6%; Score 144; DB 3; Length 107;  
Best Local Similarity 38.9%; Pred. No. 3.3e-10;  
Matches 35; Conservative 17; Mismatches 34; Indels 4; Gaps 3;

QY 31 VKIEVLHREPCSKTSKGGDLNAHYDGLAKDSKFCSTONEGHPKFWLVGQVITK 90  
DB 2 VKIDRI-SPGDGATFPKTDGLVTHYTGTL-ENGQKF--DSSVDRGSPFOCNIGVGVIK 57  
QY 91 GLDIAMTDMCPGEKRVVIPPSPFAYGKEGY 120  
DB 58 GMDVGIPKLSVGEKARLTIPGPYAVGPRGF 87

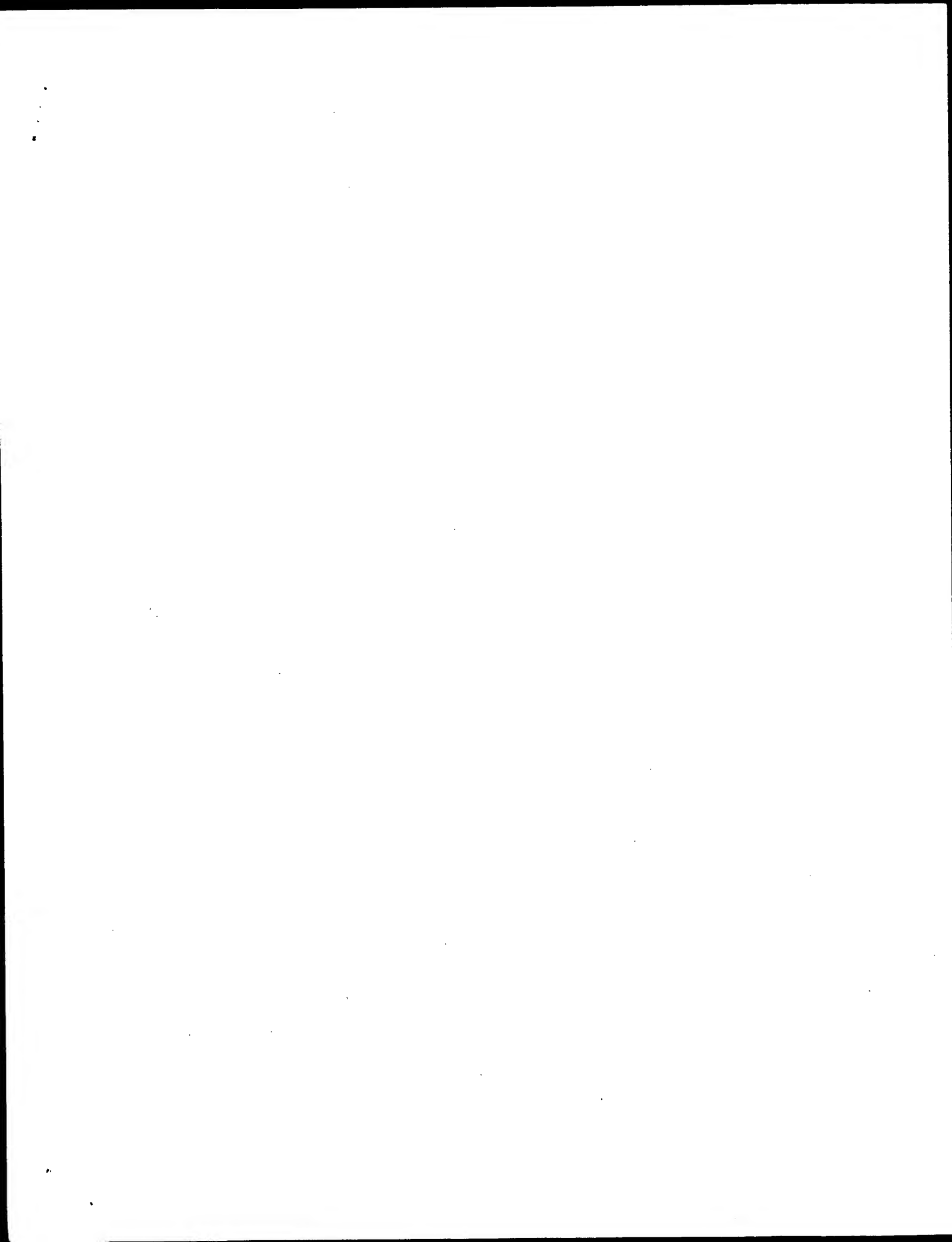
RESULT 15  
US-08-894-173-79  
Sequence 79, Application US/08894173A  
Patent No. 6090612  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
TITLE OF INVENTION: Adenylate cyclase and uses therefor  
FILE REFERENCE: P14716C  
CURRENT APPLICATION NUMBER: US/08/894,173A  
CURRENT FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 79  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Yeast  
US-08-894-173-79

Query Match 20.6%; Score 144; DB 3; Length 107;  
Best Local Similarity 38.9%; Pred. No. 3.3e-10;  
Matches 35; Conservative 17; Mismatches 34; Indels 4; Gaps 3;

QY 31 VKIEVLHREPCSKTSKGGDLNAHYDGLAKDSKFCSTONEGHPKFWLVGQVITK 90  
DB 2 VKIDRI-SPGDGATFPKTDGLVTHYTGTL-ENGQKF--DSSVDRGSPFOCNIGVGVIK 57  
QY 91 GLDIAMTDMCPGEKRVVIPPSPFAYGKEGY 120  
DB 58 GMDVGIPKLSVGEKARLTIPGPYAVGPRGF 87

Search completed: August 31, 2001, 12:05:50  
Job time: 105 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:05 ; Search time 14.47 seconds

(without alignments)  
679.096 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLFRFLVFFYLMGLTAQ.....PPSFAYGKEGYDKPLAKGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 205.5 | 29.4        | 139    | T21882 | hypothetical prote |
| 2          | 204.5 | 29.3        | 261    | T31741 | hypothetical prote |
| 3          | 199.5 | 28.6        | 140    | T49668 | binding protein -  |
| 4          | 199.5 | 28.6        | 142    | JC1365 | FK506/rapamycin-bi |
| 5          | 186.5 | 26.7        | 163    | S71238 | probable peptidylp |
| 6          | 182   | 26.1        | 581    | T49669 | FKBP65 binding pro |
| 7          | 180   | 25.8        | 151    | T12090 | probable peptidylp |
| 8          | 178.5 | 25.6        | 146    | S71237 | probable peptidylp |
| 9          | 178   | 25.5        | 134    | UT0748 | FK506-binding prot |
| 10         | 176.5 | 25.3        | 135    | S25337 | probable peptidylp |
| 11         | 175   | 25.1        | 262    | T42709 | peptidylprolyl iso |
| 12         | 172.5 | 24.7        | 264    | T29780 | hypothetical prote |
| 13         | 158.5 | 22.7        | 259    | T27586 | hypothetical prote |
| 14         | 153.5 | 22.0        | 201    | S75144 | hypothetical prote |
| 15         | 147.5 | 21.1        | 124    | JN0320 | FKBP-type peptidyl |
| 16         | 145   | 20.8        | 132    | B75347 | rapamycin-binding  |
| 17         | 144   | 20.6        | 114    | A33146 | peptidyl-prolyl ci |
| 18         | 142.5 | 20.4        | 215    | A40050 | peptidylprolyl iso |
| 19         | 142.5 | 20.4        | 392    | S55971 | probable peptidylp |
| 20         | 142   | 20.3        | 120    | S11090 | FK506-binding prot |
| 21         | 141   | 20.2        | 551    | S72485 | peptidylprolyl iso |
| 22         | 139.5 | 20.0        | 105    | M40211 | FK506-inhibitable  |
| 23         | 139.5 | 20.0        | 224    | J01522 | peptidylprolyl iso |
| 24         | 137.5 | 19.7        | 487    | T10215 | hypothetical prote |
| 25         | 135.5 | 19.4        | 108    | S54139 | FK506-binding prot |
| 26         | 135.5 | 19.4        | 411    | S48647 | peptidylprolyl iso |
| 27         | 134   | 19.2        | 559    | S55383 | peptidylprolyl iso |
| 28         | 133.5 | 19.1        | 109    | B20222 | peptidylprolyl iso |
| 29         | 133.5 | 19.1        | 109    | F81245 | FKBP-type peptidyl |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 133   | 19.1 | 107 | 2 | A61431 | peptidylprolyl iso |
| 31 | 132.5 | 19.0 | 457 | 2 | JC5422 | FK506-binding prot |
| 32 | 131   | 18.8 | 458 | 1 | A42386 | hsp 90-binding pro |
| 33 | 130   | 18.6 | 108 | 2 | A35780 | peptidylprolyl iso |
| 34 | 130   | 18.6 | 108 | 2 | A42657 | FK506-binding prot |
| 35 | 129.5 | 18.6 | 412 | 2 | A55320 | immunophilin FKBP4 |
| 36 | 128.5 | 18.4 | 112 | 2 | T40724 | peptidyl-prolyl ci |
| 37 | 128.5 | 18.4 | 357 | 2 | JC4090 | FK506-binding 39k  |
| 38 | 128   | 18.3 | 568 | 2 | T06489 | probable peptidylp |
| 39 | 124   | 17.8 | 108 | 2 | JH0528 | FK506-binding prot |
| 40 | 124   | 17.8 | 123 | 1 | A43328 | peptidylprolyl iso |
| 41 | 124   | 17.8 | 458 | 2 | JN0873 | immunophilin p59 - |
| 42 | 123.5 | 17.7 | 79  | 2 | S39850 | FKBP immunophilin  |
| 43 | 122.5 | 17.6 | 240 | 2 | A64403 | peptidylprolyl iso |
| 44 | 122   | 17.5 | 459 | 2 | A46372 | immunophilin FKBP5 |
| 45 | 120   | 17.2 | 159 | 2 | T46954 | peptidylprolyl iso |

#### ALIGNMENTS

RESULT 1

T21882

hypothetical protein F36H1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000

C:Accession: T21882

R:Kershaw, J.

submitted to the EMBL Data Library, January 1996

A:Reference number: 219482

A:Accession: T21882

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-139 <MIL>

A:Cross-references: EMBL:Z68760; PIDDN:CAA92994.1; GSPDB:GN00022; CESP:F36H1.1

A:Experimental source: clone F36H1

C:Genetics:

A:Gene: CESP:F36H1.1

A:Map position: 4

A:Introns: 43/2: 80/3

C:Superfamily: BKR-type peptidylprolyl isomerase; BKR-type peptidylprolyl isomerase

F:45-92/Domain: BKR-type peptidylprolyl isomerase homology <PPI>

Query Match 29.4%; Score 205.5; DB 2; Length 139;

Best Local Similarity 46.3%; Pred. No. 4,7e-13;

Matches 44; Conservative 16; Mismatches 32; Indels 3; Gaps 2;

OY 25 ESTSEVKEIVLHREPNCSTKSKGDLNAHYDGLAKDSKFCSTONGHPKWEVLG 84

DB 21 ECKIDKLDIGVKKRAENCVRKSGDQDLMHMYTGTL-DGTEFDSRTNNEFT--FTLG 77

OY 85 VGOVTKGLDIAMTDMCPGCKRRVYIPPSFAYGKEG 119

DB 78 GGNVTKGMDGLNKCVRERILITPPLGTEGNG 112

RESULT 2

T31741

hypothetical protein C05C8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 02-Sep-2000

C:Accession: T31741

R:Sammons, L.; Wohldmann, P.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid C05C8.

A:Reference number: 221078

A:Accession: T31741

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-261 <SAM>

A:Cross-references: EMBL:AF016430; PIDDN:AA865370.1; GSPDB:GN00023; CESP:C05C8.3

A:Experimental source: strain Bristol N2; clone C05C8

C:Genetics:  
 A:Gene: CESP:C05C8.3  
 A:Map position: 5  
 A:Introns: 119/3  
 C:Superfamily: BKBp-type peptidylprolyl isomerase homology <PPI>  
 F:48-94/Domain: BKBp-type peptidylprolyl isomerase homology <PPI2>  
 F:166-213/Domain: BKBp-type peptidylprolyl isomerase homology <PPI2>

Query Match 29.3%; Score 204.5; DB 2; Length 261;  
 Best Local Similarity 44.5%; Pred. No. 1.2e-12;  
 Matches 49; Conservative 15; Mismatches 43; Indels 3; Gaps 2;

QY 10 FFYLMGLFTAQROKKESTEVEKIEVLHREPCNSKTSKGGDLNAHYDGLAKDGSFYSRTONGCHPKFVILGV 69  
 DB 127 FVELKSTIFRPPKPAWITDEGVHITHHEVEGCTEKRAQAGDTLHOQYTLNL-EDGSFIDS 185

QY 70 SRQNGCHPKFVILGVGOVYKGLDIAMTDMCPGKRRKRVIPPSFAYGKEG 119  
 DB 186 SMSRN--RPEIFRMGSGQVYKGMIDMEGMCQGEKRRKRVIPPELAYGENG 233

RESULT 3  
 149668  
 binding protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I49668  
 R:Hendrickson, B.A.; Zhang, W.; Craig, R.J.; Jin, Y.  
 Gene 134, 271-275, 1993  
 A:Title: Structural organization of the genes encoding human and murine FK506-binding pr  
 A:Reference number: I49668; MUID:94085790  
 A:Accession: I49668  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-140 <RES>  
 A:Cross-references: GB:M7831; NID:9433782; PIDN:AAA7631.1; PID:9433783  
 C:Genetics:  
 A:Gene: FKBP13  
 A:Introns: 55/3; 93/2; 109/1; 121/1  
 C:Superfamily: BKBp-type peptidylprolyl isomerase; BKBp-type peptidylprolyl isomerase ho  
 F:47-94/Domain: BKBp-type peptidylprolyl isomerase homology <PPI>

Query Match 28.6%; Score 199.5; DB 2; Length 140;  
 Best Local Similarity 46.8%; Pred. No. 1.8e-12;  
 Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

QY 26 ESTEEVKIEVLHREPCNSKTSKGGDLNAHYDGLAKDGSFYSRTONGCHPKFVILGV 85  
 DB 24 EGKRLQIGVKKRVDPICSRKGDVLMHMTGKL-EDGTEFDSLPQNG--PVEFSLGT 80

QY 86 GOVYKGLDIAMTDMCPGKRRKRVIPPSFAYGKEG 119  
 DB 81 GOVYKGMQGLGMCCEGKRRKRVIPSELGYGGERG 114

RESULT 4  
 JCI365  
 FK506/rapamycin-binding protein FKBP13 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-Aug-1998  
 C:Accession: JCI365; A39602  
 R:Dilella, A.G.; Hawkins, A.; Craig, R.J.; Schreiber, S.L.; Griffin, C.A.  
 Biochem. Biophys. Res. Commun. 189, 819-823, 1992  
 A:Title: Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13.  
 A:Reference number: JCI365; MUID:93112052  
 A:Accession: JCI365  
 A:Molecule type: DNA  
 A:Residues: 1-142 <DL>  
 R:Jin, Y.J.; Albers, M.W.; Lane, W.S.; Brierer, B.E.; Schreiber, S.L.; Burakoff, S.J.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6677-6681, 1991  
 A:Title: Molecular cloning of a membrane-associated human FK506- and rapamycin-binding p

A:Reference number: A39602; MUID:91319747

A:Accession: A39602  
 A:Molecule type: mRNA  
 A:Residues: 1-20, '5', 23-142 <JIN>  
 A:Cross-references: GB:M65128  
 C:Genetics:

A:Gene: GDB:FKBP2  
 A:Cross-references: GDB:133728; OMIM:186946  
 A:Map position: 11q13.1-14q13.3  
 A:Introns: 57/3; 95/2; 111/1; 123/1  
 C:Superfamily: BKBp-type peptidylprolyl isomerase; BKBp-type peptidylprolyl isomerase  
 C:Keywords: immunoregulation  
 F:1-22/Domain: signal sequence  
 F:23-142/Product: FK506/rapamycin-binding protein FKBP13 #status predicted <SIG>  
 F:49-96/Domain: BKBp-type peptidylprolyl isomerase homology <PPI>

Query Match 28.6%; Score 199.5; DB 2; Length 142;  
 Best Local Similarity 46.8%; Pred. No. 1.9e-12;  
 Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

QY 26 ESTEEVKIEVLHREPCNSKTSKGGDLNAHYDGLAKDGSFYSRTONGCHPKFVILGV 85  
 DB 26 EGKRLQIGVKKRVDPICSRKGDVLMHMTGKL-EDGTEFDSLPQNG--PVEFSLGT 82

QY 86 GOVYKGLDIAMTDMCPGKRRKRVIPPSFAYGKEG 119  
 DB 83 GOVYKGMQGLGMCCEGKRRKRVIPSELGYGGERG 116

RESULT 5  
 S71238  
 probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliana  
 N:Alternate names: FK-binding protein 15-2; Immunophilin  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: S71238  
 R:luan, S.; Kudla, J.; Grunsem, W.; Schreiber, S.L.  
 submitted to the EMBL Data Library, March 1996  
 A:Description: Molecular characterization of a FKBP-type immunophilin from higher pla  
 A:Reference number: S71238  
 A:Accession: S71238  
 A:Molecule type: mRNA  
 A:Residues: 1-163 <LUA>  
 A:Cross-references: EMBL:U52047; NID:91272407; PIDN:AAC49391.1; PID:91272408  
 C:Genetics:  
 A:Gene: FKBP15-2  
 C:Superfamily: BKBp-type peptidylprolyl isomerase; BKBp-type peptidylprolyl isomerase  
 C:Keywords: cis-trans-isomerase  
 F:52-99/Domain: BKBp-type peptidylprolyl isomerase homology <PPI>

Query Match 26.7%; Score 186.5; DB 2; Length 163;  
 Best Local Similarity 36.6%; Pred. No. 4.1e-11;  
 Matches 49; Conservative 16; Mismatches 48; Indels 21; Gaps 5;

QY 7 FIVFFYLMGL--FTAQROKKESTEVEKIEVLHREPCNSKTSKGGDLNAHYDGLAKD 64  
 DB 12 FLIFFLSLISLOGFA---KKTGDVSPFLQIGVKKRPTCEVQAHKDDITKVHRTGKIT-DG 66

QY 65 SKRYCSTONGCHPKFVILGVGOVYKGLDIAMTDMCPGKRRKRVIPPSFAYGKEG----- 119  
 DB 67 TVP--DSSEFERGDPPEFKLGSQVYKGMQGLGACVGEKRRKRLKIPAKLIGEGSGSPPTI 124

QY 120 -----YDKPLLA 126  
 DB 125 PGATATLFTETELA 138

RESULT 6  
 I49669  
 FKBP6 binding protein - mouse  
 C:Species: Mus musculus (house mouse)









Fri Aug 31 12:10:25 2001

us-09-622-522-1.rpt

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:55 ; Search time 23.08 Seconds

(without alignments)  
739.487 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698

Sequence: 1 MHFLFRFIVFFYLMGLFTFAQ.....PPSFAYGKRGYDKPILAKGI 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_UNCLASSIFIED:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_VIRUS:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 653   | 93.6        | 259    | 4 Q9Y680  | Q9Y680 homo sapien |
| 2          | 648   | 92.8        | 222    | 4 Q9Y680  | Q9Y680 homo sapien |
| 3          | 553   | 79.2        | 218    | 11 O54998 | O54998 mus musculu |
| 4          | 271.5 | 38.9        | 211    | 4 Q9Y680  | Q9Y680 homo sapien |
| 5          | 223   | 31.9        | 216    | 5 Q9Y680  | Q9Y680 homo sapien |
| 6          | 220   | 31.5        | 216    | 5 Q9Y680  | Q9Y680 homo sapien |
| 7          | 206.5 | 29.6        | 137    | 5 Q9Y680  | Q9Y680 homo sapien |
| 8          | 205.5 | 29.4        | 139    | 5 Q9Y680  | Q9Y680 homo sapien |
| 9          | 204.5 | 29.3        | 261    | 5 Q9Y680  | Q9Y680 homo sapien |
| 10         | 196.5 | 28.2        | 138    | 5 Q9Y680  | Q9Y680 homo sapien |
| 11         | 193.5 | 27.7        | 137    | 5 Q9Y680  | Q9Y680 homo sapien |
| 12         | 193.5 | 27.7        | 137    | 5 Q9Y680  | Q9Y680 homo sapien |
| 13         | 190   | 27.2        | 481    | 4 Q9Y680  | Q9Y680 homo sapien |
| 14         | 189.5 | 27.1        | 137    | 5 Q9Y680  | Q9Y680 homo sapien |
| 15         | 187.5 | 26.9        | 517    | 4 Q9Y680  | Q9Y680 homo sapien |
| 16         | 187.5 | 26.9        | 570    | 11 Q9Y680 | Q9Y680 homo sapien |
| 17         | 187   | 26.8        | 582    | 4 Q9Y680  | Q9Y680 homo sapien |
| 18         | 186.5 | 26.7        | 163    | 10 Q9Y680 | Q9Y680 homo sapien |
| 19         | 186.5 | 26.7        | 163    | 10 Q9Y680 | Q9Y680 homo sapien |

|    |       |      |     |           |                     |
|----|-------|------|-----|-----------|---------------------|
| 20 | 180   | 25.8 | 151 | 10 Q41649 | Q41649 vicia faba   |
| 21 | 179.5 | 25.7 | 150 | 11 Q9JHX5 | Q9JHX5 mus musculu  |
| 22 | 178.5 | 25.6 | 146 | 10 Q38935 | Q38935 arabidopsis  |
| 23 | 178.5 | 25.6 | 153 | 10 Q9LSP4 | Q9LSP4 arabidopsis  |
| 24 | 178   | 25.5 | 134 | 5 Q17280  | Q17280 botryllus s  |
| 25 | 177.5 | 25.4 | 577 | 13 Q9YIC3 | Q9YIC3 gallus gall  |
| 26 | 175   | 25.1 | 262 | 4 Q9UE89  | Q9UE89 homo sapien  |
| 27 | 175   | 25.1 | 355 | 4 Q9H6J3  | Q9H6J3 homo sapien  |
| 28 | 172.5 | 24.7 | 264 | 5 P91180  | P91180 caenorhabdi  |
| 29 | 166.5 | 23.9 | 164 | 5 Q908J8  | Q908J8 brugia mala  |
| 30 | 163.5 | 23.4 | 201 | 4 Q9NYL4  | Q9NYL4 homo sapien  |
| 31 | 162   | 23.2 | 119 | 13 Q9DFL8 | Q9DFL8 gilllichthys |
| 32 | 158.5 | 22.7 | 259 | 5 Q23338  | Q23338 caenorhabdi  |
| 33 | 157.5 | 22.6 | 578 | 10 Q9FJL3 | Q9FJL3 synecocyst   |
| 34 | 153.5 | 22.0 | 201 | 2 P73037  | P73037 synecocyst   |
| 35 | 145   | 20.8 | 152 | 2 Q9RTG6  | Q9RTG6 deinococcus  |
| 36 | 141   | 20.2 | 551 | 10 Q38931 | Q38931 arabidopsis  |
| 37 | 141   | 20.2 | 551 | 10 Q38949 | Q38949 arabidopsis  |
| 38 | 141   | 20.2 | 555 | 10 Q9LSP3 | Q9LSP3 arabidopsis  |
| 39 | 137.5 | 19.7 | 108 | 5 Q9Y8S8  | Q9Y8S8 drosophila   |
| 40 | 137.5 | 19.7 | 487 | 10 Q9STK2 | Q9STK2 arabidopsis  |
| 41 | 137   | 19.6 | 143 | 10 Q9ELB3 | Q9ELB3 arabidopsis  |
| 42 | 129.5 | 18.6 | 108 | 5 Q904Z3  | Q904Z3 manduca sex  |
| 43 | 129.5 | 18.6 | 457 | 6 Q9XSH5  | Q9XSH5 salmella bol |
| 44 | 128.5 | 18.4 | 208 | 10 Q9SCY2 | Q9SCY2 arabidopsis  |
| 45 | 128.5 | 18.4 | 349 | 5 Q9YF88  | Q9YF88 drosophila   |

## ALIGNMENTS

|                       |   |                    |                   |
|-----------------------|---|--------------------|-------------------|
| RESULT 1              | PRELIMINARY:  | PRT:               | 259 AA.           |
| Q9Y680                | Q9Y680  |                    |                   |
| AC                    | Q9Y680  |                    |                   |
| DT                    | 01-NOV-1999 (TREMBLrel. 12, Created)                              |                    |                   |
| DT                    | 01-NOV-1999 (TREMBLrel. 12, Last sequence update)                 |                    |                   |
| DT                    | 01-MAR-2001 (TREMBLrel. 16, Last annotation update)               |                    |                   |
| DE                    | FK506-BINDING PROTEIN FRB23 ISOFORM.                              |                    |                   |
| OS                    | Homo sapiens (Human).   |                    |                   |
| OC                    | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;           |                    |                   |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |                    |                   |
| OX                    | NCBI_TaxID=9606;  |                    |                   |
| RM                    | [1]   |                    |                   |
| RP                    | SEQUENCE FROM N.A.  |                    |                   |
| RC                    | TISSUE-PIUTARY TUMOR:   |                    |                   |
| RA                    | Guan Z., Zhang Q., Dai M., Song H., Mao Y., Wu X., Mao M., Fu G., |                    |                   |
| RT                    | Luo M., Chen J., Hu R.,   |                    |                   |
| RT                    | "Human FK506-binding Protein (FKBP23)-isoform gene."              |                    |                   |
| RL                    | Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.           |                    |                   |
| CC                    | -I- SIMILARITY: TO EF-HAND FAMILY.                                |                    |                   |
| DR                    | EMBL: AF100751; AADA3015.1; -                                     |                    |                   |
| DR                    | HSSP: P20081; IYAT.   |                    |                   |
| DR                    | InterPro: IPR000866; -  |                    |                   |
| DR                    | InterPro: IPR001179; -  |                    |                   |
| DR                    | InterPro: IPR002048; -  |                    |                   |
| DR                    | Pfam: PF00036; ehand; 2.  |                    |                   |
| DR                    | Pfam: PF00254; FKBP; 2.   |                    |                   |
| DR                    | PROSITE: PS00018; EF_HAND; UNKNOWN 2.                             |                    |                   |
| DR                    | PROSITE: PS00014; EF_TARGET; UNKNOWN 1.                           |                    |                   |
| DR                    | PROSITE: PS00454; FKBP_PPIASE_2; UNKNOWN 1.                       |                    |                   |
| DR                    | PROSITE: PS00059; FKBP_PPIASE_3; 1.                               |                    |                   |
| KW                    | Calcium-binding.  |                    |                   |
| SO                    | SEQUENCE 259 AA; 30009 MW; 886A1F3F5ACB9E78 CRC64;                |                    |                   |
| Query Match           | 93.6%;  | Score 653;         | DB 4; Length 259; |
| Best local similarity | 100.0%;   | Pred. No. 3.1e-61; |                   |
| Matches 120;          | Conservative 0;   | Mismatches 0;      | Indels 0; Gaps 0; |
| OY                    | 1 MHFLFRFIVFFYLMGLFTFAQRRKEESTEEVKEIVLHRPENCSTSKGDLNHHYGYL 60     |                    |                   |
| DB                    | 5 MHFLFRFIVFFYLMGLFTFAQRRKEESTEEVKEIVLHRPENCSTSKGDLNHHYGYL 64     |                    |                   |

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QY 61 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 65 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 124

RESULT 2
QY6B0 PRELIMINARY; PRT; 222 AA.
AC QY6B0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FK506-BINDING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-NORMAL PITUITARY;
RA Han Z., Song H., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G.,
RA Luo M., Chen J., Hu R.;
RT "Human FK506-binding protein mRNA, complete cds.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AF092137; AAD40379.1; -.
DR HSSP; AF092137; AAD40379.1; -.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Calcium-binding.
SQ SEQUENCE 222 AA; 25768 MW; 376C4CBB78DF730D CRC64;

Query Match 92.8%; Score 648; DB 4; Length 222;
Best local similarity 99.2%; Pred. No. 8,7e-61;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHFLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60
|||||
DB 5 MHFLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 64

QY 61 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 65 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 124

RESULT 3
QY6B0 PRELIMINARY; PRT; 218 AA.
AC QY6B0;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FK506-BINDING PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIH/SWISS;
RA Nakamura T., Yabe D., Kanazawa N., Tashiro K., Sasayama S., Honjo T.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: TO EF-HAND FAMILY.

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DR EMBL; AF040252; AAC79959.1; -.
DR HSSP; P20081; 1YAT
DR MGI; MGI:1336879; FKBP7.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 218 AA; 24913 MW; DB0AE509560EEBA CRC64;

Query Match 79.2%; Score 553; DB 11; Length 218;
Best local similarity 85.8%; Pred. No. 9.6e-51;
Matches 103; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MHFLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60
|||||
DB 1 MHFLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60

QY 61 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 61 AKDSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120

RESULT 4
QY6B0 PRELIMINARY; PRT; 211 AA.
AC QY6B0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ20731 FIS, CLONE HEP10272.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Odayashi M.,
RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AK000738; BAA91351.1; -.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Calcium-binding.
SQ SEQUENCE 211 AA; 24172 MW; 858184954FE10029 CRC64;

Query Match 38.9%; Score 271.5; DB 4; Length 211;
Best local similarity 44.2%; Pred. No. 5.7e-21;
Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

QY 3 FLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 62
|||||
DB 4 FLRFVFFYLMGLFTAQROKKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 58

QY 63 DGSKFCYCSRTQNEGHPKFWVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGYDK 122
|||||

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Db 59 DGSJFHSHTNNQPIWFTLGLTLEALKMDQGLKMGCVGEKRLIIPALGYGKEGK 118

RESULT 5  
ID 09X254 PRELIMINARY; PRT: 216 AA.

DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE BCDNA:GM07659.  
GN FKBP13 OR BCDNA:GM07659 OR BCDNA:GH08925 OR CG9847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M.,  
RA Lewis S.E., Sun C., Rubin G.M.;  
RT "Full Length Drosophila melanogaster cDNA sequence."  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL: AF132555; AAD27854.1; -  
DR HSSP: P20081; 1YAT  
DR PiyBase: FBgn010470; FKbp13.  
DR InterPro: IPR000886; -  
DR InterPro: IPR001179; -  
DR InterPro: IPR002048; -  
DR Pfam: PF00036; ehand; 2.  
DR Pfam: PF00254; FKBP; 1.  
DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE: PS00059; FKBP\_PPIASE\_3; 1.  
DR SMART: SM00054; Efh; 1.  
DR SMART: SM00054; Efh; 1.  
DR Calcium-binding.  
KW  
SQ SEQUENCE 216 AA; 23960 MW; E1AEAD276766C9C8 CRC64;

Query Match 31.9%; Score 223; DB 5; Length 216;  
Best Local Similarity 49.5%; Pred. No. 7.9e-16;  
Matches 45; Conservative 12; Mismatches 32; Indels 2; Gaps 1;

QY 29 EVKIVLHREPCSKTSKKGDLNHYGYLAKDGSKRYCSTQNEGHPKMFVLGGOV 88  
DB 24 EDLKEVISTPEVCEQSKNSKNDSLTMHYTGLQADGKKFDSFDRDQ--PFTFLGAGOV 81  
QY 89 IKGLDAMTDMPGPKRKVYVPPSFAYGKGG 119  
DB 82 IKGMDOGGLNMCYGEKRLITIPOLGYGDOG 112

RESULT 6  
ID 09V3V2 PRELIMINARY; PRT: 216 AA.

AC 09V3V2;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE FKBP13 PROTEIN.  
GN FKBP13 OR BCDNA:GM07659 OR BCDNA:GH08925 OR CG9847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA  
RC STRAIN-BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Abmayri A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Genter A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merulov G., Milshina N.V., Modarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon R., Nusskern D.R., Paclebo J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan M., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tsang G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,  
RA Agbayani A., Arcaina T.T., Baxter E., Blazer R.G., Butenoff C.,  
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.B., Frise E.,  
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,  
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Paclebo J.M.,  
RA Park S., Sequeira A., Sethi H., Snir E., Svitskas R.R., Weinburg T.,  
RA Celniker S.E.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL: AE003454; AAF46726.1; -  
DR EMBL: AF132154; AAD34742.1; -  
DR HSSP: P20081; 1YAT.  
DR PiyBase: FBgn010470; FKbp13.  
DR InterPro: IPR000886; -  
DR InterPro: IPR001179; -  
DR InterPro: IPR002048; -  
DR Pfam: PF00036; ehand; 2.  
DR Pfam: PF00254; FKBP; 1.  
DR PROSITE: PS00018; EF\_HAND; 2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE: PS00059; FKBP\_PPIASE\_3; 1.  
DR SMART: SM00054; Efh; 1.  
DR SMART: SM00054; Efh; 1.  
DR Calcium-binding; Hypothetical protein.  
KW  
SQ SEQUENCE 216 AA; 23960 MW; 5A8501C02DDA2E80 CRC64;

Query Match 31.5%; Score 220; DB 5; Length 216;  
Best Local Similarity 48.4%; Pred. No. 1.6e-15;  
Matches 44; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

QY 29 EVKIVLHREPCSKTSKKGDLNHYGYLAKDGSKRYCSTQNEGHPKMFVLGGOV 88  
DB 24 EDLKEVISTPEVCEQSKNSKNDSLTMHYTGLQADGKKFDSFDRDQ--PFTFLGAGOV 81

Qy 89 IKGLDIAMTDMCPGKRRKVVIPSPFAYGREG 119  
 Db 82 IKGMDOGLINMCYGEKRLITIPPLGVDG 112

RESULT 7  
 ID 096335 PRELIMINARY; PRT; 137 AA.  
 AC 096335;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE PPTIDYL-PROLYL CIS-TRANS ISOMERASE.  
 GN FKBP13.  
 OS Brugia malayi.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Brugia.  
 OC NCBI\_TaxID=6279;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT Ma D., Hong X.Q., Carlow C.R.S.;  
 RT "A FK506-insensitive small molecular weight FKBP of filarial  
 parasites."  
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF016454; AAD01595.1; -  
 DR HSSP; P20071; 1FKU.  
 DR InterPro; IPR001179; -  
 DR Pfam; PF00254; FKBP; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 DR Isomerase.  
 KW SEQUENCE 137 AA; 15270 MW; 0F3E0C363768D91E CRC64;  
 SQ

Query Match 29.4%; Score 206.5; DB 5; Length 137;  
 Best Local Similarity 45.3%; Pred. No. 2.5e-14;  
 Matches 43; Conservative 18; Mismatches 31; Indels 3; Gaps 2;

Oy 25 EESTEEVKIEVLHPENCSTKSKGDDLNAHYDGLAKDSKFCSTQNEGHKMPVLG 84  
 Db 20 DKEARLQIGVKRRVDCERSRGGDLNHYVGM-EDGETFDSRRNK--PFTTLG 76  
 Oy 85 VGOVTKGLDIAMTDMCPGKRRKVVIPSPFAYGREG 119  
 Db 77 MGQVTKGMDOGLINMCYGEKRLITIPPLGVDG 111

RESULT 8  
 ID 020107 PRELIMINARY; PRT; 139 AA.  
 AC 020107;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE F36H1.1 PROTEIN.  
 GN F36H1.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT Kershaw J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Latreille P.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RT Nature 368:32-38(1994).  
 RL EMBL; Z68760; CAA92994.1; -  
 DR HSSP; P18203; 1ERL.  
 DR InterPro; IPR001179; -  
 DR Pfam; PF00254; FKBP; 1.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 SQ SEQUENCE 139 AA; 15472 MW; A1AE973BD0ED5F6 CRC64;

Query Match 29.4%; Score 205.5; DB 5; Length 139;  
 Best Local Similarity 46.3%; Pred. No. 3.3e-14;  
 Matches 44; Conservative 16; Mismatches 32; Indels 3; Gaps 2;

Oy 25 EESTEEVKIEVLHPENCSTKSKGDDLNAHYDGLAKDSKFCSTQNEGHKMPVLG 84  
 Db 21 EOKIDKIQIGVKRRVDCERSRGGDLNHYTGL-DGETFDSRRNK--PFTTLG 77  
 Oy 85 VGOVTKGLDIAMTDMCPGKRRKVVIPSPFAYGREG 119  
 Db 78 QGNVTKGMDOGLINMCYGEKRLITIPPLGVDG 112

RESULT 9  
 ID 016309 PRELIMINARY; PRT; 261 AA.  
 AC 016309;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE C05C8.3 PROTEIN.  
 GN C05C8.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Latreille P.,  
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 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
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 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
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 RT Nature 368:32-38(1994).  
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 RC STRAIN=BRISTOL N2;  
 RA Sammons L., Wohlmann P.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016430; AAB65370.1; -  
 DR HSSP; P27124; 1ROT.









